

F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984

F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP) //8.6e-158:771:97//Hs.155481:AJ006470

F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus] //1.9e-62:384:89//Hs.115498:AA436298

F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092

F-NT2RP4000263

F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580

F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481

F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732

F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112

F-NT2RP4000355

F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195

F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae] //1.2e-09:157:76//Hs.97950:AI382073

F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678

F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368

F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688
F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
//0.014:178:66//Hs.125315:AF027156
F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete
cds//2.0e-34:431:73//Hs.46468:U45984
F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:7
5//Hs.154326:D42087
F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468
F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:
J03853
F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-spec
ific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499
F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151
:AB001535
F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//
Hs.78862:D87742
F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete
cds//0.94:133:69//Hs.159234:U89995
F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2
//0.60:335:61//Hs.74605:X13293
F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594
F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904
F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partia
l//2.0e-34:203:93//Hs.99423:AJ010840
F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66/
/Hs.100837:AB002372
F-NT2RP4000524
F-NT2RP4000528
F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154

F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus] //1.1e-27:162:93//Hs.25597:H93026

F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351

F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053

F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730

F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513

F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396

F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907

F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848

F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783

F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens] //2.8e-46:411:78//Hs.111817:T80622

F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178

F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440

F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058

F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162

F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123

F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939

F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:

438:99//Hs.8173:AC005189

F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833

F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603

F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278

F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367

F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803

F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843

F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142

F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901

F-NT2RP4000918

F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503

F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532

F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371

F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542

F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888

F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058

F-NT2RP4000979

F-NT2RP4000984

F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds

//0.85:257:63//Hs.12956:U90913
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs
 .79706:U53204
 F-NT2RP4001004
 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-
 90:425:99//Hs.126082:AI077718
 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, par
 tial cds//2.8e-19:689:61//Hs.113287:AF009204
 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-
 84:778:74//Hs.154970:U03494
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete
 cds//0.95:170:64//Hs.2864:L40157
 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP
)//7.2e-13:441:63//Hs.155481:AJ006470
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497
 F-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase,
 partial//1.4e-131:634:98//Hs.106778:AJ010953
 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternat
 ive products} //0.025:166:66//Hs.146459:X66975
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5
 e-85:604:86//Hs.13273:AB011164
 F-NT2RP4001095
 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:44
 8:98//Hs.105837:AA536054
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
 ALPHA SUBUNIT [Canis familiaris]//2.2e-26:171:92//Hs.14038:R06800
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//H

s.109804:D64142

F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:100//Hs.126925:AA931237

F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.143382:AA476266

F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261

F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207

F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171

F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734

F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324

F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264

F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324

F-NT2RP4001207

F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636

F-NT2RP4001213//KRAB zinc finger protein {alternative products} //1.1e-45 :187:74//Hs.22556:U37251

F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262

F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.122967:AF059569

F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs .106387:AF029778

F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463

F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59k D, acidic component)//0.015:246:62//Hs.31121:U40571

F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578

F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs .110826:U80736

F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40

) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250
F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917
F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110
F-NT2RP4001339
F-NT2RP4001343
F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625
F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445
F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356
F-NT2RP4001372
F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194
F-NT2RP4001375
F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190
F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918
F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109
F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957
F-NT2RP4001433//Zinc finger protein 10 (K0X 1)//1.1e-88:839:73//Hs.2479:X78933
F-NT2RP4001442
F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326
F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.26676:AA033997

F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//
Hs.75533:D10523

F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN
[H.sapiens] //0.25:216:60//Hs.63220:AA522707

F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395

F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:
281:61//Hs.5923:X82260

F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:17
3:94//Hs.5570:AI377863

F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-
35:329:76//Hs.154970:U03494

F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds
//0.0015:221:65//Hs.44481:U13220

F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs
.30649:U50534

F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174

F-NT2RP4001567

F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN
MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83/
/Hs.158208:AA167836

F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410

F-NT2RP4001574

F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98
//Hs.108826:AL031228

F-NT2RP4001592

F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903

F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952

F-NT2RP4001634

F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN

FKH1-STH1 INTERGENIC REGION [S.cerevisiae] //8.6e-57:287:97//Hs.117439:C
18436

F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.55
91:AB000409

F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MI
TOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae] //1.0:311:59//Hs.57969:A
A203629

F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-ma
f) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376

F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:33
2:86//Hs.113283:AF018080

F-NT2RP4001696

F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927

F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, comp
lete cds//0.0035:247:62//Hs.92614:M62302

F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//
Hs.1285:U08198

F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M
27878

F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656

F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-3
4:400:68//Hs.154212:AC004522

F-NT2RP4001803//Human high conductance inward rectifier potassium channe
l alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069

F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131

F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//
3.1e-07:509:59//Hs.1572:U11690

F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:7

3//Hs.78398:D31888
 F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.
 6e-57:813:65//Hs.6336:AB014572
 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170
 F-NT2RP4001889
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:
 97//Hs.15144:AC005014
 F-NT2RP4001896
 F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848
 F-NT2RP4001927
 F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien
 s]//2.8e-54:375:84//Hs.119294:AI379442
 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894
 F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063
 F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868
 F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25.
 Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (l
 ymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal prot
 ein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains EST
 s and GSSs//1.7e-54:788:65//Hs.23796:AL022718
 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete
 cds//0.0019:279:65//Hs.159439:AF092047
 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila
 melanogaster]//0.58:463:55//Hs.3826:U69560
 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139
 F-NT2RP4002052
 F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873

F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA
, complete cds//0.97:227:60//Hs.100030:AF002999

F-NT2RP4002075

F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapie
ns] //1.0e-38:243:90//Hs.139115:AA325104

F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654

F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152
:70//Hs.25180:M96684

F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0
e-10:401:59//Hs.89616:M55284

F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204

F-NT2RP4002888

F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960

F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96
//Hs.74456:U34995

F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071

F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 s
ubunit//0.18:271:60//Hs.139745:U39067

F-NT2RP5003492

F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase
, complete cds//6.1e-56:750:69//Hs.132884:AB006179

F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5
.1e-14:348:62//Hs.154050:AC004131

F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.9
4:202:63//Hs.8152:AB014542

F-NT2RP5003522

F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943

F-NT2RP5003534

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0

e-69:373:94//Hs.108258:AB007934
 F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729
 F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata] /
 /4.4e-75:355:99//Hs.36727:AI051983
 F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304
 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:81
 5:98//Hs.81449:AF058922
 F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//H
 s.113264:AB005060
 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:23
 8:89//Hs.69469:AF064603
 F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549
 F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapi
 ens] //6.7e-60:305:97//Hs.31696:H50008
 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798
 F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543
 F-OVARC1000085
 F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442
 F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete cds//0.00017:414:59
 //Hs.106387:AF029778
 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600
 F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans] //2.9e-73:406
 :92//Hs.109463:AI205174
 F-OVARC1000109
 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48
 -18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250
 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.
 4e-43:532:72//Hs.118401:AB011134
 F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010

F-OVARC1000139
 F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293
 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
 F-OVARC1000151
 F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
 F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136
 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131
 F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
 F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
 F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379
 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984
 F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868
 F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
 F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
 F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]//0.51:193:66//Hs.6194:AI378579
 F-OVARC1000321
 F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946
 F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
 F-OVARC1000347
 F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450

F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64/
/Hs.156016:D50930
F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58/
/Hs.156016:D50930
F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:19
0:84//Hs.139513:AA259082
F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93:281:60//Hs.7
6279:X53416
F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//
Hs.83987:U09284
F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423
F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.
2e-140:566:99//Hs.12334:AB014583
F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524
F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.1
08112:AF070640
F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854
F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926
F-OVARC1000479
F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036
F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327
F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:53
9:99//Hs.111285:AF051850
F-OVARC1000526//ESTs//2.9e-08:368:61//Hs.42771:N26740
F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492
F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475

F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667
 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA,
 complete cds//0.87:135:66//Hs.85302:U76421
 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358
 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200
 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63/
 /Hs.3080:U29725
 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722
 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881
 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-
 7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.
 6e-100:536:94//Hs.111862:AB011162
 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106
 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279
 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
 //4.8e-153:549:99//Hs.125315:AF027156
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs
 .4764:AB018306
 F-OVARC1000700
 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltra
 nsferase mRNA, complete cds//1.2e-110:451:91//Hs.13476:AF038661
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]
 //2.9e-53:318:91//Hs.7049:AI141736

F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411
 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H
 .sapiens] //1.2e-38:194:99//Hs.157059:W28130
 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793
 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835
 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584
 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032
 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9
 e-151:432:100//Hs.155995:AB014543
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//H
 s.18910:AF045584
 F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus] //6
 .1e-31:183:93//Hs.108620:AA418155
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete
 cds//0.54:133:69//Hs.159234:U89995
 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143
 F-OVARC1000885//EST//0.91:152:63//Hs.160765:AI313323
 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777
 F-OVARC1000890
 F-OVARC1000891
 F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818
 F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3
 e-85:419:97//Hs.9028:AF039691
 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456
 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//
 4.3e-64:623:72//Hs.114440:M11119

F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078
 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H. sapiens] //2.4e-29:157:97//Hs.136243:AA307843
 F-OVARC1000948
 F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986
 F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952
 F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288
 F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069
 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661
 F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.155302:U57317
 F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:AF088219
 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114
 F-OVARC1001004
 F-OVARC1001010
 F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus] //3.8e-47:234:99//Hs.110327:AA205866
 F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75063:AL023584
 F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus] //3.9e-97:578:89//Hs.111974:AI050735
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149
 F-OVARC1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074
 F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385
 F-OVARC1001051
 F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete

cds//1.1e-46:381:81//Hs.154968:U02020
 F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873
 F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:18
 3:84//Hs.46680:AA809451
 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial
 cds//6.6e-132:620:98//Hs.3426:AF082657
 F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013
 F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937
 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X982
 48
 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone I
 MAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berl
 in))//1.3e-75:289:95//Hs.21753:AJ005897
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//
 Hs.12912:AF015913
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.
 1e-151:710:98//Hs.26584:AF051782
 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102
 F-OVARC1001118
 F-OVARC1001129
 F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008
 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725
 F-OVARC1001162
 F-OVARC1001167
 F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279
 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287
 F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159
 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 P
 RECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581

F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//
Hs.91103:AC005551

F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]
//1.5e-13:199:71//Hs.109966:C06057

F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN
VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:
W72675

F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889

F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688

F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676

F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825

F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837

F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821

F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224

F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8
e-144:644:96//Hs.155995:AB014543

F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:35
5:60//Hs.108812:AA044835

F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172

F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, c
omplete cds//0.20:188:64//Hs.152455:AF044209

F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264

F-OVARC1001330

F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (eryt
hrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531

F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:36
3:99//Hs.105837:AA536054

F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493

F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251
 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete c
 ds//0.64:198:61//Hs.105940:AF004715
 F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633
 F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777
 F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4
 e-69:533:74//Hs.109299:AB014554
 F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
 lete cds//2.5e-49:365:73//Hs.129735:AF010144
 F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involve
 d in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819
 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA
 , complete cds//0.097:235:65//Hs.25674:AF072242
 F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225
 F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//
 Hs.21586:AB006651
 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586
 :69//Hs.74597:U52426
 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651
 F-OVARC1001436
 F-OVARC1001442
 F-OVARC1001453
 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN
 TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.1109
 50:AI041823
 F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568
 F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343
 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete
 cds//2.6e-86:479:92//Hs.6534:AF016507

F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-9
7:538:92//Hs.75813:L33243

F-OVARC1001525

F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786

F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595

F-OVARC1001555

F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA/
/6.8e-57:275:98//Hs.155160:AF031166

F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:AI144299

F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:21
6:99//Hs.120002:AI038398

F-OVARC1001611

F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500

F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3
e-37:217:94//Hs.14409:AB011144

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e
-49:393:81//Hs.95582:AB006867

F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229

F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.4
28:U03858

F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807

F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863

F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80
//Hs.155652:X06825

F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588

F-OVARC1001762

F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eI
F3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670

F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575

F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:AI218697

F-OVARC1001791

F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830

F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102

F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287

F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172

F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825

F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453

F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567

F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537

F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973

F-OVARC1001861

F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611

F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709

F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127

F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953

F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749

F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834

F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261

F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.8904
0:U48263

F-OVARC1001928

F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//
Hs.79706:U53204

F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK6
52.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794

F-OVARC1001949//KRAB zinc finger protein {alternative products} //1.8e-17
:294:67//Hs.22556:U37251

F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228

F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639

F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776

F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417

F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6
e-160:739:98//Hs.108258:AB007934

F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865

F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063

F-OVARC1002107

F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7
e-101:498:96//Hs.75258:AF054174

F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913

F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399
:62//Hs.112725:AF056022

F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795

F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097

F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:3
29:58//Hs.107747:AI357868

F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.

00010:300:64//Hs.118929:X79568
 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:17
 8:64//Hs.108447:AJ000517
 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
 F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA,
 partial cds//1.2e-52:550:72//Hs.42400:AF022789
 F-PLACE1000014
 F-PLACE1000031
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
 F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755
 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499
 F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cdna yk1
 0c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771
 F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING E
 NTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366
 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30
 :324:60//Hs.76460:U49082
 F-PLACE1000094
 F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo
 sapiens]//6.2e-82:476:92//Hs.111081:AI380378
 F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]/
 /7.7e-27:205:85//Hs.9670:AA632135
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, compl
 ete cds//2.5e-151:737:97//Hs.151017:AF058291
 F-PLACE1000185
 F-PLACE1000213
 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255

F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226

F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022

F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202

F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294

F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047

F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675

F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197

F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153

F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024

F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516

F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260

F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174

F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053

F-PLACE1000424

F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590

F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531

F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638

F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60/

/Hs.153014:AB002353
 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289
 F-PLACE1000562
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//
 Hs.21838:AF038179
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD/
 /2.3e-85:503:88//Hs.62661:M55542
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e
 -165:798:97//Hs.159597:AJ012449
 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.9
 8:215:60//Hs.8152:AB014542
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986
 F-PLACE1000636
 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
 complete cds//5.0e-154:747:96//Hs.5819:AF102265
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone I
 MAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.2959
 5:AJ005896
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1)
 mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353
 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:
 70//Hs.47313:D87447
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:33

1:57//Hs.37110:U10694
 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858
 F-PLACE1000769
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215
 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000
 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201
 F-PLACE1000948
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821
 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk2.8h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:AB018267
 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6

940:Z48633

F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876

F-PLACE1001024

F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741

F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204

F-PLACE1001062

F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859

F-PLACE1001088

F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485

F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817

F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:71//Hs.150406:AF022158

F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704

F-PLACE1001168

F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135

F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741

F-PLACE1001238

F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494

F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929

F-PLACE1001272//COATOMER BETA' SUBUNIT//0.012:50:96//Hs.75724:X70476

F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283

F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164

F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930

F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:37
0:60//Hs.42672:AF016052

F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385

F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591

F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8
e-26:155:95//Hs.61638:AB018342

F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44
:393:79//Hs.152005:AF009615

F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748

F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA
, complete cds//2.6e-09:117:84//Hs.21301:AF093419

F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR
KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646

F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, co
mplete CDS//0.0038:496:57//Hs.97681:AJ223333

F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mR
NA//7.0e-45:456:75//Hs.154069:U06452

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//
6.5e-71:365:96//Hs.110404:AF091087

F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232

F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987

F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510

F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455

F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716

F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529

F-PLACE1001503

F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914

F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753

F-PLACE1001545
 F-PLACE1001551
 F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835
 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005
 F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690
 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:AB018341
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198
 F-PLACE1001640
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927
 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250
 F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696
 F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776
 F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686
 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094
 F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.

1480:M60052

F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159

F-PLACE1001745

F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/
/2.8e-160:773:97//Hs.4812:AF061243

F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-3
5:269:83//Hs.5247:AF029750

F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283

F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, comp
lete cds//3.4e-52:548:72//Hs.150981:U47050

F-PLACE1001781

F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115

F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta s
ubunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953

F-PLACE1001821

F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494

F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214

F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906

F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257

F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220

F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cd
s//4.0e-153:685:95//Hs.17839:AF099936

F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837

F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58
//Hs.106387:AF029778

F-PLACE1001989

F-PLACE1002004

F-PLACE1002046

F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465
:58//Hs.153322:D42108

F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555

F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2
e-39:635:64//Hs.38176:AB011178

F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA
, complete cds//4.3e-83:388:99//Hs.5171:AF069765

F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637

F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.
2e-13:384:61//Hs.737:M62831

F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSO
R [Homo sapiens]//0.89:60:75//Hs.144290:T61747

F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631

F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:7
9//Hs.40100:AB002390

F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891

F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627

F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674

F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.9079
8:U79289

F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989

F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442

F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935

F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3
e-75:434:83//Hs.23094:M19503

F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675

F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279

F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291
 F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710
 F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067
 F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.40993:AF000148
 F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947
 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158
 F-PLACE1002465
 F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581
 F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523
 F-PLACE1002493
 F-PLACE1002499
 F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010
 F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:AB018256
 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:AC004774
 F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369
 F-PLACE1002571//Homo sapiens mRNA for TP53, complete cds//0.99:274:59//Hs.138202:AF027866
 F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627
 F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725
 F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497

F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187
F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915
F-PLACE1002625
F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04
412
F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180
F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903
F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971
F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827
F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516
F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926
F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
F-PLACE1002815
F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163
F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167
F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405
F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029
F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056

F-PLACE1002962

F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus] /
/0.031:372:59//Hs.8021:AI041815

F-PLACE1002991

F-PLACE1002993

F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans] //1.3e-12:104
:86//Hs.124808:T86959

F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0510//0.99:192:64//Hs.92660:AB007979

F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0
e-131:632:97//Hs.129872:AB011088

F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7
e-14:555:58//Hs.154740:AB014567

F-PLACE1003045

F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491

F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//
Hs.102137:U31875

F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419

F-PLACE1003136

F-PLACE1003145

F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590

F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997

F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797

F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransfe
rase mRNA, complete cds//0.98:221:60//Hs.139756:U59209

F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532

F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770

F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208

F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:6

2//Hs.85112:X57025

F-PLACE1003256

F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802

F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106

F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376

F-PLACE1003334

F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308

F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568

F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715

F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277

F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575

F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858

F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009

F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069

F-PLACE1003383

F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546

F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178

F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like) //0.40:206:62//Hs.30223:X90846

F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912

F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874

F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635

F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//

3.4e-85:357:86//Hs.103948:K00627
 F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145
 F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6
 940:Z48633
 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248
 F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:54
 3:97//Hs.120416:AA057428
 F-PLACE1003553
 F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780
 F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:4
 99:58//Hs.65993:AF000367
 F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932
 F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194
 F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENT
 RY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620
 F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965
 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.896
 50:L38961
 F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97
 //Hs.56851:D83200
 F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00
 065:236:64//Hs.22116:AF064104
 F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3
 e-122:737:87//Hs.23094:M19503
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.
 021:445:58//Hs.158275:AI365413

F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56/
/Hs.76730:AB002299

F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1
.4e-133:669:95//Hs.98658:AF053305

F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101

F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor pro
tein//8.5e-09:393:60//Hs.103527:AJ000553

F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien
s]//1.8e-53:260:99//Hs.102928:AI346344

F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648

F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983

F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
2.7e-40:608:68//Hs.139107:K00629

F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944

F-PLACE1003783

F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0
:457:57//Hs.62318:AB018308

F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:3
14:60//Hs.1050:M85169

F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201
:68//Hs.40806:AA018786

F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165

F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124

F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359

F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257

F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770

F-PLACE1003886

F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:70
2:67//Hs.153322:D42108

F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCH
 ONDRIAL PRECURSOR [*Saccharomyces cerevisiae*]//1.2e-49:251:98//Hs.65831:F
 03069
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit m
 RNA, complete cds//2.0e-47:522:71//Hs.3136:U42412
 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812
 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration o
 ncogene spil//0.85:164:64//Hs.153045:X52056
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta pol
 ypeptide 1//3.1e-41:422:74//Hs.3620:X04526
 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [*C.elegans*]//8.2e-82:418
 :96//Hs.156161:AI333779
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64/
 /Hs.76986:D83785
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precu
 sor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273

F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689

F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R. norvegicus] //1.1e-98:479:97//Hs.31718:N29128

F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914

F-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830

F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884

F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576

F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588

F-PLACE1004336

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153

F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans] //3.9e-109:521:98//Hs.14079:AA306552

F-PLACE1004384//Human HsLIM15 mRNA for HsLim15, complete cds//2.0e-49:466:76//Hs.37181:D64108

F-PLACE1004388

F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871

F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579

F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190

F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete

cds//9.9e-131:536:99//Hs.155410:U49283
 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867
 F-PLACE1004460
 F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363
 F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085
 F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416
 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163
 F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680
 F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445
 F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150
 F-PLACE1004518
 F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
 F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854
 F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299
 F-PLACE1004645
 F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991
 F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
 F-PLACE1004664
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606
 F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589
 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561

F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.
48483:AF007131

F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:9
6:71//Hs.125740:AA884845

F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542

F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891

F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148

F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680

F-PLACE1004743

F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,
4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:2
60:90//Hs.6863:W52470

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-1
72:828:97//Hs.104715:AF084367

F-PLACE1004777//Human myosin-IXb mRNA, complete cds//1.0e-29:556:63//Hs.
159629:U42391

F-PLACE1004793

F-PLACE1004804

F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340

F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTE
IN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284

F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:
69//Hs.22111:AB002362

F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047

F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943

F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:33
8:57//Hs.8546:U97669

F-PLACE1004838

F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//

0.89:200:66//Hs.21537:X80910
 F-PLACE1004868
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772
 F-PLACE1004900
 F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382
 F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929
 F-PLACE1004918//Human tumor susceptiblity protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936
 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592
 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
 F-PLACE1004969
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147
 F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520
 F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831
 F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459
 F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159
 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943
 F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569
 F-PLACE1005077//EST//0.79:283:59//Hs.89276:AA283899
 F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740

F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147

F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401

F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561

F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366

F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227

F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661

F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:H11741

F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087

F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:AB014541

F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:A1138605

F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417

F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009

F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//Hs.47334:W72370

F-PLACE1005243

F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252

F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:AB011182

F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66
//Hs.101642:X60673
F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//
0.83:239:62//Hs.80684:X62534
F-PLACE1005313
F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.eleg
ans] //6.0e-81:459:91//Hs.146177:R51650
F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:8
8//Hs.134031:AC004794
F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.9
6:510:56//Hs.159183:AB018297
F-PLACE1005373
F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348
F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.740
95:L20433
F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925
F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5
e-126:744:87//Hs.23094:M19503
F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323
F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973
F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385

F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144

F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PRO
TEIN L2 PRECURSOR [*Saccharomyces cerevisiae*]//4.5e-51:258:97//Hs.7736:W8
1261

F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278

F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472
:U48436

F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594

F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851

F-PLACE1005611//ESTs, Weakly similar to B0035.14 [*C.elegans*]//3.5e-32:19
7:92//Hs.8241:AA283057

F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234

F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867

F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991

F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete
cds//2.1e-151:721:98//Hs.8765:AF083255

F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74/
/Hs.75319:X59618

F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.
086:223:59//Hs.27349:AB007917

F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:37
4:85//Hs.23759:M98457

F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437

F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944

F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding mo
tif, complete cds//0.75:289:59//Hs.75111:D87258

F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:37
7:62//Hs.162:X16302

F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIO

ESTERASE, MEDIUM CHAIN [Rattus norvegicus] //5.7e-49:252:88//Hs.24309:AI1
25696

F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493

F-PLACE1005802

F-PLACE1005803

F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
//4.5e-128:636:96//Hs.125315:AF027156

F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//
8.4e-156:739:98//Hs.11183:AF065482

F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens] //4.1e-42:327:81//Hs.138404:R70986

F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58/
/Hs.75770:L41870

F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497

F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905

F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242

F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487

F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552

F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300

F-PLACE1005898

F-PLACE1005921

F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504

F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274

F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342
:57//Hs.89839:M18391

F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142

F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:
X69978

F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357

F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468
F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:
66//Hs.107747:AI357868
F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, co
mplete cds//1.0:215:63//Hs.7885:U13948
F-PLACE1005968
F-PLACE1005990
F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:
312:77//Hs.42674:U61981
F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256
F-PLACE1006011
F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743
F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.
021:202:64//Hs.158319:AB018332
F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97
//Hs.98782:X99906
F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395
F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//
4.1e-147:679:99//Hs.4976:AF039023
F-PLACE1006129
F-PLACE1006139
F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:
79//Hs.153014:AB002353
F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.
sapiens]//2.9e-12:119:84//Hs.23153:R92857
F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868
F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:9
2//Hs.152894:AC005239

F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:
99//Hs.30464:AF091433
F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608
F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation fac
tor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719
F-PLACE1006205
F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH F
ACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:AI279486
F-PLACE1006225
F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668
F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185
F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802
F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3
e-168:791:98//Hs.31921:AB014548
F-PLACE1006262
F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.
7277:AJ001625
F-PLACE1006318
F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503
F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492
F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249
F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481
F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.
153529:AF070581
F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete c
ds//2.6e-07:403:61//Hs.105940:AF004715
F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693
F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:9

7//Hs.22396:AF062085

F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:

74//Hs.21560:AB002296

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129

F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866

F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470

F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194

F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511

F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493

F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584

F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542

F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358

F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219

F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784

F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529

F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280

F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670

F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088
F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858
F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63/
/Hs.26956:L40396
F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473
F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]
//1.6e-12:113:83//Hs.3385:N25917
F-PLACE1006678
F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153
638:AF010403
F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1
.6e-05:382:63//Hs.43627:U35612
F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354
F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152
F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M
97252
F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783
F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228
F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10
:84:95//Hs.123642:M83941
F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017
F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892
F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.
47:403:56//Hs.15832:AB014518
F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7
e-103:619:87//Hs.23094:M19503
F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876
F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773
F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273

F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.
0:268:58//Hs.5333:AB018254

F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601

F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187

F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443

F-PLACE1006917

F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913

F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211

F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565

F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723

F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cer
evisiae]//3.2e-07:67:98//Hs.21806:AA630312

F-PLACE1006962//H.sapiens irlB mRNA//2.3e-16:202:71//Hs.135202:X63417

F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c
) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922

F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753

F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei
(ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102

F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971

F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0
e-117:775:84//Hs.23094:M19503

F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.1298
11:AJ223957

F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:3
61:60//Hs.75813:L33243

F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987

F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glyco
gen debranching enzyme, glycogen storage disease type III)//0.18:268:63/
/Hs.904:U84010

F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385
F-PLACE1007112
F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121
F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78
869:M81601
F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965
F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090
:412:59//Hs.8546:U97669
F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64
//Hs.79706:U53204
F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-
II-T1, complete cds//2.0e-58:405:87//Hs.80598:D50495
F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467
F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//
Hs.121556:Y15909
F-PLACE1007274
F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syn
drome)//0.94:167:64//Hs.606:L06133
F-PLACE1007282
F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436
F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA,
complete cds//0.88:298:58//Hs.144877:AF029403
F-PLACE1007342
F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mR
NA, complete cds//1.7e-121:567:98//Hs.76596:AF096870
F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77/
/Hs.19949:X98173

F-PLACE1007375

F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642

F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287

F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//Hs.14387:AF093771

F-PLACE1007416

F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436

F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359

F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93/
/Hs.6445:L40391

F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714

F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975

F-PLACE1007488

F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385

F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503

F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296

F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979

F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:5
7//Hs.113283:AF018080

F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755

F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.
0e-70:733:71//Hs.65238:AB014561

F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863

F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257

F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163

F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2
e-12:778:56//Hs.33010:AB014533

F-PLACE1007621

F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867
 F-PLACE1007645
 F-PLACE1007649
 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266
 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63
 //Hs.1103:X02812
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.757
 89:D87953
 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/
 /4.1e-149:709:97//Hs.4812:AF061243
 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //4.5e-36:233:89//Hs.108797:AA476815
 F-PLACE1007729//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE
 [H.sapiens] //0.00033:270:64//Hs.104129:AA923278
 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.
 6e-156:728:98//Hs.153121:AB014585
 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:6
 8//Hs.159347:M62424
 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030
 F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469
 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656
 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504
 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107
 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841
 F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635
 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3
 e-38:396:77//Hs.23094:M19503

F-PLACE1007852

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.
3e-190:894:98//Hs.28020:AB018309

F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387

F-PLACE1007877

F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//7.3e-156:755:97//Hs.92381:AB007956

F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002

F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, com
plete cds//8.9e-173:813:98//Hs.5671:AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds//8.2e-155:730:98//Hs.78106:AF079529

F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapi
ens] //5.1e-45:264:92//Hs.42222:W28567

F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043

F-PLACE1008000//Homo sapiens veli 1 mRNA, complete cds//5.7e-63:578:74//
Hs.150380:AF087693

F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031

F-PLACE1008044

F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382

F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0
.00037:151:71//Hs.159437:U44060

F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds
//1.0:461:58//Hs.155494:U60975

F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, comp
lete cds//0.034:497:58//Hs.100431:AF044197

F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769

F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:AI263135
 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524
 F-PLACE1008201
 F-PLACE1008209
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856
 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385
 F-PLACE1008273
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970
 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129
 F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911
 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171
 F-PLACE1008398

F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA
 , complete cds//2.5e-09:461:62//Hs.25674:AF072242

F-PLACE1008402//Homo sapiens mRNA for pl15, complete cds//1.4e-149:711:9
 8//Hs.7763:D86326

F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943

F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-2
 6.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro
 /X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contai
 ns ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.5792
 2:AL023653

F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499

F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, ep
 idermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]//0.019:530:58
 //Hs.72248:S72487

F-PLACE1008437

F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335

F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901

F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63
 //Hs.27590:AB002381

F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds/
 /6.8e-07:469:60//Hs.1177:U10886

F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TAS
 K) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823

F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697

F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-
 45:507:71//Hs.8003:AC004997

F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.
 0:95:71//Hs.117546:U31767

F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:AB018334
 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087:AA649326
 F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794
 F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560
 F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458
 F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211
 F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333
 F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728
 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406
 F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741
 F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080
 F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:AF060543
 F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772
 F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542
 F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905

F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883

F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858

F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728

F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563

F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503

F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308

F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771

F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026

F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937

F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308

F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950

F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112

F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762

F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689

F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585

F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698

F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525

F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800

F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091

F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031

F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011
 F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890
 F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788
 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3
 (XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:
 59//Hs.35804:D25215
 F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:44
 0:78//Hs.37181:D64108
 F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//4.0e-46:440:69//Hs.158095:AB007953
 F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, comp
 lete cds//0.28:245:61//Hs.92614:M62302
 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
 F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770
 F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821
 F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //3.6e-117:588:95//Hs.54943:Z78396
 F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689
 F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
 F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.1
 46403:M29540
 F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Sa
 ccharomyces cerevisiae] //1.9e-21:121:98//Hs.124768:AA307735
 F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mR
 NA, complete cds//9.7e-08:411:59//Hs.23731:U83192

F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3
e-91:594:86//Hs.23094:M19503

F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767

F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473

F-PLACE1009368

F-PLACE1009375

F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81/
/Hs.43681:AL022394

F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M
27878

F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101
174:AF047863

F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:2
10:86//Hs.3404:AF035262

F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:
68//Hs.155291:D13630

F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:5
8//Hs.82128:AJ012159

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.
76987:AF012872

F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.1
51641:Z24680

F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS
E BETA 2//0.00039:347:60//Hs.994:M95678

F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//4.
1e-91:464:96//Hs.155049:AC004531

F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839

F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:
63//Hs.16165:AB002405

F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728

F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417

F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956

F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866

F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291

F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806

F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394

F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011

F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085

F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773

F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087

F-PLACE1009639

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159

F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534

F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926

F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789

F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024

F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989

F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996

F-PLACE1009845

F-PLACE1009861

F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021

F-PLACE1009886

F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889

F-PLACE1009908

F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717

F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379

F-PLACE1009925

F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153

F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446

F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345

F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114

F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540

F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529

F-PLACE1010023

F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878

F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H. sapiens] //5.2e-63:312:98//Hs.142151:AA984061

F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482

F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925

F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus] //1.8e-38:212:95//Hs.98067:AA236822

F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R. norvegicus] //1.8e-08:100:89//Hs.11469:U69567

F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569

F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682

F-PLACE1010134//H. sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889

F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740

F-PLACE1010152

F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792

F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582

F-PLACE1010202//ESTs, Weakly similar to No definition line found [C. elegans] //2.3e-72:391:94//Hs.35225:H69637

F-PLACE1010231

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917

F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590

F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149
:93//Hs.11449:AI201540

F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813

F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74
095:L20433

F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:
U76248

F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659

F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117

F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855

F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648

F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986

F-PLACE1010401

F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61/
/Hs.125257:U70824

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete c
ds//7.2e-152:702:99//Hs.13313:AF039081

F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500

F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100

F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein m
RNA, complete cds//1.0:175:64//Hs.159273:AF054177

F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472

F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979

F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148

F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA
HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229
:N44661

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14

p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61
 //Hs.106387:AF029778
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//
 0.012:258:62//Hs.144375:AA484200
 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5
 e-66:363:95//Hs.10801:AB011102
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076
 F-PLACE1010662
 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, com
 plete cds//1.1e-74:697:74//Hs.37138:U35376
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mR
 NA, partial cds//6.1e-77:393:96//Hs.50758:AF092564
 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), pa
 rtial//0.97:314:59//Hs.14574:AJ131244
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.
 159629:U42391
 F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTE
 IN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTE
 IN HCNGP [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140
 F-PLACE1010786
 F-PLACE1010800
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157

F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085
F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1
[H.sapiens] //2.9e-28:245:79//Hs.132736:AA583494
F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048
F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel.
[H.sapiens] //5.8e-67:336:97//Hs.130135:AA905493
F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:
X59244.
F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7
e-149:694:98//Hs.118087:AB011182
F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:1
67:65//Hs.1050:M85169
F-PLACE1010900
F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981
F-PLACE1010917
F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537
F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1
e-139:653:98//Hs.74750:AB011126
F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//
2.9e-91:437:98//Hs.66392:AF064244
F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985
F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154
F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59/
/Hs.585:X04506
F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632
F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721
F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931
F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032

F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds/
/0.28:179:67//Hs.1177:U10886

F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE
E BETA 2//6.2e-11:207:68//Hs.994:M95678

F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-
35:310:78//Hs.2407:Z49194

F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk)
mRNA, complete cds//0.74:228:61//Hs.153640:U56998

F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320

F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663

F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037

F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317

F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857

F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949

F-PLACE1011160

F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443

F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114

F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase
mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664

F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:4
69:99//Hs.8241:AA283057

F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEE
SL70F [C.elegans]//2.6e-62:221:88//Hs.101821:W27452

F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751

F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4
e-147:675:99//Hs.23168:AB011101

F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:9
8//Hs.15144:AC005014

F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803

F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:AF070637

F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915

F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160

F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310

F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265

F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.159897:AB007970

F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535

F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Ra w3 [R.norvegicus]//6.7e-68:325:99//Hs.107245:AA627053

F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868

F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:AB011102

F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503

F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204

F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482

F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264

F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997

F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319

F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476

F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333

F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180

F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462

F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778

F-PLACE1011641

F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631

F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661

F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086

F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745

F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234

F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366

F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350

F-PLACE1011725

F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853

F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891

F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240

F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693

F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660

F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664

F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775

F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152

F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913
 F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:4
 78:56//Hs.107747:AI357868
 F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817
 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//
 3.7e-140:664:98//Hs.3838:AF059617
 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763
 F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514
 F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591
 F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514
 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0
 e-148:690:98//Hs.88756:AB018256
 F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0487//6.5e-54:290:81//Hs.92381:AB007956
 F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503
 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330
 F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627
 F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831
 F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627
 F-PLACE2000017
 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose
 polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557
 F-PLACE2000030
 F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.8
 5:234:66//Hs.11342:U91512
 F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.0
 58:348:62//Hs.94653:AB011179
 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59/
 /Hs.79706:U53204

F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
F-PLACE2000061
F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:6
62:86//Hs.23759:M98457
F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7
.1e-135:631:98//Hs.9443:AF027219
F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333
F-PLACE2000100
F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219
F-PLACE2000111//H.sapiens mRNA for 1-acylglycerol-3-phosphate O-acyltran
sferase//0.76:215:65//Hs.6587:U56417
F-PLACE2000115
F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:
79//Hs.153014:AB002353
F-PLACE2000132
F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapi
ens] //1.2e-08:245:64//Hs.140343:AA718911
F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U546
45
F-PLACE2000164
F-PLACE2000170
F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179
F-PLACE2000176
F-PLACE2000187
F-PLACE2000216
F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:
63//Hs.21560:AB002296

F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338

F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958

F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522

F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560

F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869

F-PLACE2000317

F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796

F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088

F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299

F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817

F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645

F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045

F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861

F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032

F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638

F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953

F-PLACE2000398

F-PLACE2000399

F-PLACE2000404

F-PLACE2000411

F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:46

3:74//Hs.113283:AF018080
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966
 F-PLACE2000427
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719
 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalact
 osaminytransferase (T2)//1.9e-20:418:64//Hs.130181:X85019
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:32
 4:81//Hs.113283:AF018080
 F-PLACE2000455//ESTs, Moderately similar to !!!!! ALU SUBFAMILY SC WARNIN
 G ENTRY !!!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082
 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107
 :X87241
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:52
 0:81//Hs.113283:AF018080
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:20
 4:73//Hs.46925:Y10262
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:
 69//Hs.101359:AB002384
 F-PLACE3000020//Prostaglandin I2 (prostacyclin) receptor (IP)//0.00081:5
 00:61//Hs.393:D38128
 F-PLACE3000029
 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRN
 A, complete cds//1.0:186:62//Hs.122752:AF026445
 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8
 e-48:283:83//Hs.23711:AB018295

F-PLACE3000121
 F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.
 0:194:59//Hs.6168:AB014603
 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
 F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016
 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871
 F-PLACE3000148
 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.
 6e-80:382:99//Hs.6336:AB014572
 F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023
 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A s
 ubunit//0.54:320:60//Hs.96253:U79666
 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.
 9e-66:319:88//Hs.153468:AB011147
 F-PLACE3000160
 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs
 .155464:AF088219
 F-PLACE3000194
 F-PLACE3000197
 F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546
 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975
 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECU
 RSOR//1.0:271:61//Hs.77522:X62744
 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216
 F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377
 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF
 F40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019
 F-PLACE3000226

F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046

F-PLACE3000244

F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858

F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650

F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944

F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770

F-PLACE3000310

F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586

F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219

F-PLACE3000331

F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545

F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741

F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULK [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355

F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194

F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514

F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441

F-PLACE3000363

F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928

F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641
 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
 F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73
 919:X81637
 F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785
 F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270
 F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715
 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541
 F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apa
 f-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263
 F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens
]//1.6e-51:260:98//Hs.122512:H61502
 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.
 00020:630:57//Hs.17585:AB018344
 F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161
 F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of comp
 lex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202
 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
 F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs
 .117572:U94888
 F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6
 e-118:331:100//Hs.105399:AB018352
 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1
 .1e-06:244:63//Hs.154050:AC004131
 F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//
 Hs.139088:AF070533
 F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, comp
 lete cds//1.4e-53:669:67//Hs.40993:AF000148

F-PLACE4000063

F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713

F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819

F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931

F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751

F-PLACE4000129

F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627

F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856

F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367

F-PLACE4000192

F-PLACE4000211

F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594

F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329

F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317

F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250

F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609

F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886

F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200

F-PLACE4000261

F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.15
5952:U88966

F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365

F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292

F-PLACE4000367

F-PLACE4000369

F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256

F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823

F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1
e-47:605:71//Hs.153026:AB014540

F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//
4.7e-33:159:81//Hs.154257:AI275982

F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3
e-45:263:92//Hs.2397:Z70200

F-PLACE4000445

F-PLACE4000450

F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874

F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71/
/Hs.80738:X52075

F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951

F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289

F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731

F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN
HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022

F-PLACE4000548

F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript
//0.0035:510:59//Hs.39163:AF000986

F-PLACE4000581

F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine
leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080

F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239
:79//Hs.109084:AI004675

F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074

F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.
5e-47:562:69//Hs.129685:AB002446

F-PLACE4000650

F-PLACE4000654

F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132

F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05
299

F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HO
MOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5
e-148:706:98//Hs.109299:AB014554

F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:
M23254

F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877

F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//H
s.3989:AB002313

F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-
35:299:81//Hs.2407:Z49194

F-THYRO1000034

F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099

F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326

F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63
//Hs.101996:AB002345

F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//
Hs.6654:AB014557

F-THYRO1000085

F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065

F-THYRO1000107

F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8
e-106:690:86//Hs.23094:M19503

F-THYRO1000121

F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//
Hs.103502:U70732

F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//2.8e-
155:732:98//Hs.87619:AF087142

F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203

F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416

F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs
.155464:AF088219

F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete
cds//1.1e-05:261:61//Hs.152936:D63475

F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:27
0:87//Hs.101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4
e-175:805:99//Hs.43445:AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.
0e-88:616:84//Hs.79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

F-THYR01000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:
U79297
F-THYR01000241//EST//0.48:102:69//Hs.160764:AI313322
F-THYR01000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M
27878
F-THYR01000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.6
1:211:64//Hs.60103:AB014590
F-THYR01000270
F-THYR01000279//ESTs//0.0020:104:72//Hs.121476:AI215500
F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:
848:98//Hs.25846:AB016068
F-THYR01000320//ESTs, Weakly similar to Similar to glutamate decarboxyla
se [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803
F-THYR01000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.8
0731:M63175
F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2
e-164:763:98//Hs.12002:AB018333
F-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds
//6.9e-34:177:84//Hs.7833:U29091
F-THYR01000368//ESTs//0.0011:55:96//Hs.34994:AA252919
F-THYR01000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.
081:240:62//Hs.118401:AB011134
F-THYR01000387//EST//3.6e-14:197:71//Hs.139399:AA416855
F-THYR01000394//ESTs, Weakly similar to No definition line found [C.eleg
ans]//5.8e-39:245:91//Hs.119095:T79413
F-THYR01000395//EST//5.8e-69:333:99//Hs.156524:AA724572
F-THYR01000401//ESTs//1.8e-24:132:98//Hs.54852:W26238
F-THYR01000438//EST//1.9e-05:217:63//Hs.115930:AA579773
F-THYR01000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.09

6:306:60//Hs.155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X5252
0

F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-2
2:248:76//Hs.162011:AA513663

F-THYRO1000488

F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298

F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120

F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protei
n 4, complete cds//0.28:229:61//Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949

F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete
cds//2.4e-168:808:97//Hs.151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2
685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081

F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125

F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
3429 nt]//1.8e-09:127:77//Hs.116007:S79267

F-THYRO1000662

F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157

F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
3429 nt]//5.7e-49:281:77//Hs.116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46

:368:57//Hs.26557:AA480380
 F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59
 //Hs.79706:U53204
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74
 //Hs.7977:AB007871
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1
 .0:209:62//Hs.19492:AF061573
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:5
 7//Hs.158132:D63481
 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC
 41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084
 F-THYRO1000787
 F-THYRO1000793
 F-THYRO1000796
 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.
 4e-36:561:68//Hs.129685:AB002446
 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:7
 5//Hs.154326:D42087
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
 F-THYRO1000843
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788
 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170
 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0487//1.8e-43:318:79//Hs.92381:AB007956
F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529
F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79
217:M77836
F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs
.112432:AC005263
F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65/
/Hs.83558:D86963
F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA he
licase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complet
e cds//2.7e-15:123:90//Hs.106469:AF042169
F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
F-THYRO1000983
F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307
F-THYRO1001003
F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124
:AF019369
F-THYRO1001033//H.sapiens mRNA for cylicin II//0.0061:287:60//Hs.3232:Z4
6788
F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.
51048:X68830
F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:
72//Hs.153014:AB002353
F-THYRO1001100//Human DNA-binding protein mRNA, 3' end//2.1e-74:741:74//H
s.159249:Z99130
F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447
:62//Hs.124024:AF053700

F-THYR01001121//ESTs//0.92:257:61//Hs.118246:N95416
 F-THYR01001133//EST//1.1e-38:367:75//Hs.144175:H70425
 F-THYR01001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
 F-THYR01001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
 F-THYR01001173
 F-THYR01001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
 F-THYR01001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
 F-THYR01001204
 F-THYR01001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.
 .155464:AF088219
 F-THYR01001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
 F-THYR01001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.
 6467:AJ002309
 F-THYR01001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
 //0.014:178:66//Hs.125315:AF027156
 F-THYR01001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836
 F-THYR01001313//ESTs//1.0:244:61//Hs.127488:AA528182
 F-THYR01001320//ESTs//0.062:126:67//Hs.133296:AI311872
 F-THYR01001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68/
 /Hs.153563:AF011333
 F-THYR01001322//ESTs//0.12:238:61//Hs.29169:N66545
 F-THYR01001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207
 F-THYR01001363//ESTs//1.0e-16:178:78//Hs.163954:N57939
 F-THYR01001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79
 //Hs.12385:AB007877
 F-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4
 e-157:740:97//Hs.138488:AB014607
 F-THYR01001401//EST//4.6e-14:171:76//Hs.157587:AI356993
 F-THYR01001403//ESTs//2.2e-50:464:79//Hs.118046:N49946

F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62
 //Hs.477:U05659
 F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' f
 lanking sequence//4.6e-33:153:81//Hs.102877:U41315
 F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71/
 /Hs.44782:Z82215
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.
 51048:X68830
 F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943
 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//
 Hs.25306:AF070572
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27
 655
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs
 .75551:L12535
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071
 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2
 e-13:108:86//Hs.141045:AA191659
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter

), member 4//0.099:540:55//Hs.95958:M91463
 F-THYR01001661//ESTs//0.12:53:92//Hs.151586:W45568
 F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59
 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089
 F-THYR01001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF0
 10238
 F-THYR01001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.
 122908:AF070552
 F-THYR01001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
 F-THYR01001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila
 melanogaster]//2.5e-51:296:92//Hs.3826:U69560
 F-THYR01001738//EST//6.9e-30:180:94//Hs.58641:W81229
 F-THYR01001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
 F-THYR01001746//EST//0.96:119:63//Hs.144107:AI053590
 F-THYR01001772//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725
 F-THYR01001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
 F-THYR01001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//
 Hs.11711:AB002295
 F-THYR01001828
 F-THYR01001854//EST//0.038:128:67//Hs.160649:AI241823
 F-THYR01001895//Intercellular adhesion molecule 1 (CD54), human rhinovir
 us receptor//9.6e-13:288:65//Hs.51061:M24283
 F-THYR01001907//EST//1.9e-12:126:80//Hs.139296:AA350198
 F-VESEN1000122
 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
 F-Y79AA1000033
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:
 230:66//Hs.431:L13689

F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:U78521

F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192

F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623

F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

F-Y79AA1000328

F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309

F-Y79AA1000346

F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs

.155464:AF088219
 F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018
 F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:AF082516
 F-Y79AA1000480
 F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871
 F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521
 F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356
 F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706
 F-Y79AA1000574//Human mRNA for GC box binding protein, complete cds//0.95:258:62//Hs.150557:D31716
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:AF091080
 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:AF060503
 F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513
 F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670
 F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969
 F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377
 F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067
 F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468
 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:AF098799
 F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:24
4:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete
cds//0.87:466:59//Hs.122967:AF059569

F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2
cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956

F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368
:99//Hs.86660:AA398644

F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA,
3' end//0.14:499:58//Hs.37288:D16815

F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gam
ma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536

F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116
:L04270

F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M238
92

F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//
Hs.79706:U53204

F-Y79AA1001023

F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:10
0//Hs.78489:U63329

F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:
772:60//Hs.82208:L46590

F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381

F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511

F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
F-Y79AA1001078
F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
F-Y79AA1001299//Human In11 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
F-Y79AA1001384
F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167

F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489

F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683

F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465

F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROT EIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447

F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744

F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659

F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851

F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398

F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783

F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109

F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583

F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244

F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385

F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526

F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302

F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877

F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191

F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620

F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//H

s.113082:AB007903

F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079

F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.0
3c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533

F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:14
2:90//Hs.103349:AI141124

F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:21
5:67//Hs.104115:X52332

F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62
//Hs.106387:AF029778

F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173

F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA,
complete cds//0.98:430:58//Hs.78501:L13720

F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382

F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611

F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943

F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-
53:348:88//Hs.18122:AI338045

F-Y79AA1002093

F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865

F-Y79AA1002115

F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395

F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:16
5:90//Hs.6473:AA853955

F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5
e-05:393:62//Hs.77864:AB014538

F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515

F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillu

s caldotenax] //2.3e-113:568:96//Hs.111637:AA305890
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans] //8.6e-33:338
 :73//Hs.26662:U55984
 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:6
 3//Hs.1560:D42045
 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1
 e-176:821:98//Hs.100729:AB014592
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2
 e-160:748:98//Hs.96731:AB014555
 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1
 e-130:622:97//Hs.30898:AB014534
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999
 F-Y79AA1002351//Human high conductance inward rectifier potassium channe
 l alpha subunit mRNA, complete cds//0.028:587:58//Hs.2363:L36069
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377
 F-Y79AA1002399
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142
 F-Y79AA1002431
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:
 263:69//Hs.55452:AC003973
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:6
 1//Hs.162:X16302

【 0 8 2 8 】

相同性検索結果データ 5.

3' 末端クローン配列に対する Human Unigene 相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータの Title、

P 値: 比較配列の長さ (base): 相同性 (%),

トップヒットデータの Accession No. の順に // で区切って記載した。

なお、同一クローンで 5' 末端配列に対応する 3' 末端配列が決定されていないものは空欄とした。相同性のスコアの P 値が 1 より大であった場合はデータは示さない。

R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F5
4F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.130
15:AA628434

R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.
83:314:61//Hs.266:U06233

R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198

R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:7
2//Hs.154326:D42087

R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340

R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329

R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788

R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases
[C.elegans]//4.4e-90:502:90//Hs.55918:AA151667

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1
e-100:514:94//Hs.27197:AB018340

R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1
e-45:435:77//Hs.153026:AB014540

R-nnnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is

novel. [H.sapiens] //7.7e-92:428:100//Hs.126925:AA931237
R-HEMBA1000158
R-nnnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans] //1.3e-05:58
:91//Hs.5570:AI377863
R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545
R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366
R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927
R-HEMBA1000201//Human Inil mRNA, complete cds//3.0e-25:137:99//Hs.155626
:U04847
R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311
R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532
R-nnnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404
R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70/
/Hs.127649:AB007874
R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.
3e-23:276:75//Hs.5737:AB007944
R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019
R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808
R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424
R-nnnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.
norvegicus] //4.9e-14:208:73//Hs.93332:AA811920
R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485
R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962
R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409
R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0
:122:67//Hs.129748:AB011099
R-nnnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323
R-nnnnnnnnnnnnn//Human Ca2+-dependent activator protein for secretion mRN
A, complete cds//8.8e-30:160:98//Hs.151301:U36448

R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024

R-nnnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238

R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560

R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460

R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243

R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629

R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857

R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938

R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960

R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460

R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878

R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248

R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920

R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:AI005282

R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700

R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140

R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189

R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143

R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014

R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349

R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316

R-HEMBA1000460
R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs
.155464:AF088219
R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is rel
ated to Drosophila melanogaster ring canel protein. [H.sapiens]//1.1e-31
:181:94//Hs.61454:AA312449
R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571
R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885
R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD
//4.0e-55:203:92//Hs.155510:U15782
R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sa
piens]//1.3e-117:550:99//Hs.99722:AI422277
R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//
Hs.91916:AF035317
R-nnnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699
R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881
R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norve
gicus]//1.8e-108:550:96//Hs.26799:W74481
R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
R-nnnnnnnnnnnnn

R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509
R-HEMBA1000592//TYROSINE-PROTEIN KINASE ITK/TSK//0.024:309:61//Hs.89519:L10717
R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136
R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235
R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590
R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390
R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922
R-HEMBA1000682//ESTs, Weakly similar to putative p150 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403
R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736
R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280
R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672
R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213
R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/

isomerases [C.elegans] //7.2e-113:572:95//Hs.28644:AI018612
R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:44
9:75//Hs.74478:U33931
R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777
R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110
R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs
.155464:AF088219
R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131
R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete
cds//1.6e-32:309:75//Hs.10458:AF088219
R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612
R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8
2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti
body IA4))//1.3e-48:284:90//Hs.103458:X53795
R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:8
7//Hs.154326:D42087
R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939
R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM
160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977
R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410
:77//Hs.154103:AF061258
R-HEMBA1000851
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)
//3.7e-33:284:80//Hs.159608:U46689
R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794
R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202
R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608
R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951

R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219

R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154

R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672

R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508

R-HEMBA1000919

R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597

R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619

R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291

R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074

R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750

R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.159187:AB007977

R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498

R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590

R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170

R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878

R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464

R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902

R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881

R-HEMBA1001007

R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764

R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:AB007937

R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:
95//Hs.58393:X05360

R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292

R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912

R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336

R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

R-nnnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616

R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4
e-21:186:79//Hs.132942:AB014521

R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886

R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813

R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X1442
0

R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0492//2.7e-21:417:64//Hs.127338:AB007961

R-HEMBA1001080

R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788

R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674

R-HEMBA1001094

R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245

R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs
.155464:AF088219

R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974

R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320

R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879
:M15530

R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341

R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265

R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs

.155464:AF088219

R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens] //1.1e-39:309:82//Hs.96337:AA225358

R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0492//0.21:238:60//Hs.127338:AB007961

R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896

R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothet
ical protein 5 [H.sapiens] //0.27:305:62//Hs.100238:U69194

R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:33
3:81//Hs.113283:AF018080

R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316

R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens] //2.9e-20:160:87
//Hs.103102:W55932

R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728

R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435

R-nnnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae] //2.4e-35:23
9:87//Hs.103919:AA159181

R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674

R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534

R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324

R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs
.155464:AF088219

R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:
89:68//Hs.20912:AB012162

R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214

R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019

R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977

R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950

R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN

FAB1-PES4 INTERGENIC REGION [*S.cerevisiae*]//1.3e-77:458:92//Hs.9398:N418

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R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259

R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:24
9:78//Hs.113283:AF018080

R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816

R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837

R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334

R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550

R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458

R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482

R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439

R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204

R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081

R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714

R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364

R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199

R-HEMBA1001415

R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:
183:82//Hs.42674:U61981

R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704

R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263

R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982

R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546

R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077

R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7
e-47:304:88//Hs.23094:M19503

R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220



分

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Separate Volume

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R-HEMBA1001463

R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:
66//Hs.36232:D80008

R-HEMBA1001478

R-HEMBA1001497

R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426

R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9
e-79:528:84//Hs.23094:M19503

R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269

R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA702493

R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723

R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270

R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348

R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs
.155464:AF088219

R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259
:62//Hs.2229:X82324

R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:4
56:77//Hs.159275:AF030880

R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030

R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652

R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63/
/Hs.146395:AB002329

R-HEMBA1001589

R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-
71:431:88//Hs.26625:W25874

R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
1.3e-73:533:82//Hs.103948:K00627

R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHA

SE [Arabidopsis thaliana] //4.5e-93:537:90//Hs.20218:AA628530
R-nnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:
362:60//Hs.132206:AF039694
R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158
R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623
R-nnnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens] //1.2e-8
6:442:95//Hs.63888:AA203398
R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554
R-HEMBA1001658
R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds
//1.3e-16:427:61//Hs.106511:AF029343
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA
, complete cds//1.4e-93:493:92//Hs.107254:AC005943
R-HEMBA1001675
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA
A, complete cds//4.2e-103:534:94//Hs.7381:AF038962
R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424
R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.
3e-98:483:96//Hs.31720:AB014598
R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960
R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095
R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL
PRECURSOR [Rattus norvegicus] //1.8e-46:236:98//Hs.132948:AA194452
R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs
.155464:AF088219
R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CO
NTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisi
ae] //7.1e-88:431:96//Hs.29203:AI344105

R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712
R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:
77//Hs.153014:AB002353
R-HEMBA1001744
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162
R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243
R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823
R-nnnnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180
:AF039019
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0500//9.0e-114:548:98//Hs.118164:AB007969
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334
R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF06
8179
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07
290
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707
R-nnnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:14
7:97//Hs.23476:AA401210
R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.

1e-109:553:96//Hs.78946:AB014517
R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative product
s} //1.9e-37:357:76//Hs.53217:Z48051
R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2
[H.sapiens] //2.3e-32:193:94//Hs.9489:R84329
R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.
66710:X96969
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128
R-HEMBA1001910
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens] //1.5e-73:347:100//Hs.30991:AA994438
R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces ce
revisiae] //5.1e-57:320:91//Hs.91251:U66685
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kina
se mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145
R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens] //2.9e-99:482:98//Hs.96849:AA879470
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:8
2//Hs.40100:AB002390
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668
R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825
R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.

2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso
log of a Rat gene) and a novel alternatively spliced gene. Contains a pu
tative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717
R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:
88//Hs.153014:AB002353
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6
e-91:448:97//Hs.5687:AJ005801
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837
R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//
Hs.1189:D38550
R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538
R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:6
4//Hs.101238:Y11312
R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.
4e-51:254:85//Hs.15731:AB011135
R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764
R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996
R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124
:AF019369
R-HEMBA1002113//Prostaglandin I2 (prostacyclin) synthase //1.4e-76:280:9
0//Hs.61333:D83402
R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e
-87:362:94//Hs.103443:AF065854
R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:9
4:100//Hs.107747:AI357868

R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X8395

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R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734

R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199

R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642

R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337

R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674

R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915

R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043

R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081

R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457

R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622

R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958

R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357

R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503

R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342

R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315

R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151

R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606

R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814

R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202

R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426

R-HEMBA1002257

R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN
VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:
W72675

R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314

R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595

R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818

R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679

R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8
e-130:642:96//Hs.6162:AB018314

R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822

R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094

R-nnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mR
NA, complete cds//3.9e-123:661:93//Hs.119023:AF092563

R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435

R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237

R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:9
1//Hs.25527:AC005954

R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-8
7:429:96//Hs.13209:AI417849

R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238:AA476267

R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:8
0//Hs.74554:D38522

R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069

R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085

R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395

R-nnnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:48
8:95//Hs.108115:AA582193

R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80/

/Hs.43681:AL022394

R-HEMBA1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs
.155464:AF088219

R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995

R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133

R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449

R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990

R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972

R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715

R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1
e-106:564:93//Hs.129928:AB007923

R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700

R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804

R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881

R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012

R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs
.32567:AF073519

R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs
.155464:AF088219

R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete
cds//1.4e-120:587:97//Hs.151411:AF075587

R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904

R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838

R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055

R-HEMBA1002621

R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.
2e-77:380:97//Hs.91338:AB018351

R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881

R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715
R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041
R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970
R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696
R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307
R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945
R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896
R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282
R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477
R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:AB018315
R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521
R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168
R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163
R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526
R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792
R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:AB011126
R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127
R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491

R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58/
/Hs.48824:D87717

R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75/
/Hs.153563:AF011333

R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709

R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320

R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cd
s//1.4e-116:559:97//Hs.28307:AF071185

R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//H
s.79706:U53204

R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013

R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.
norvegicus]//4.3e-25:137:98//Hs.5337:AA243757

R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514

R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830

R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827

R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670

R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, com
plete cds//1.2e-107:541:95//Hs.33787:AF037261

R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71/
/Hs.95140:D80011

R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820

R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:8
8//Hs.154326:D42087

R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481

R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165

R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679

R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732

R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892

R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085

R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124
:AF019369

R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405

R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3
e-30:162:99//Hs.5734:AB014579

R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs
.155464:AF088219

R-nnnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064

R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptid
e 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:AI377682

R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:29
0:85//Hs.113283:AF018080

R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480

R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577

R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827

R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366

R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTE
IN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5
.6e-34:280:79//Hs.114905:AA088442

R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-sub
unit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182

R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627

R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF0
10238

R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903

R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:43
4:99//Hs.14146:W92235

R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402

R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249

R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219

R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223

R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//Hs.104800:AA709155

R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624

R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058

R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.118717:U86751

R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845

R-HEMBA1003136//ESTs, Weakly similar to MANNOSYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615

R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670

R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933

R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389

R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000

R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804

R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540

R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943

R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265

R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817

R-HEMBA1003222//ESTs, Weakly similar to weak similarity to HSP90 [C.eleg

ans] //1.1e-42:310:85//Hs.23294:W27666
R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864
R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929
R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219
R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392
R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785
R-HEMBA1003281
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537-protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109
R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266
R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353
R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872
R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869
R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119
R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029
R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357
R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540
R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651

R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588
R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247
R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//1.8e-11:261:65//Hs.87578:AI125363
R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847
R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127
R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204
R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563
R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013
R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:5
44:98//Hs.25812:AF058696
R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121
R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:52
9:84//Hs.113283:AF018080
R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sa
piens]//2.8e-93:495:93//Hs.91619:AA552351
R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058
R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [
H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440
R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//

Hs.46918:AF052099
R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212
R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087
R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042
R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374
R-HEMBA1003615
R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167
R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888
R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021
R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438
R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830
R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010
R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783
R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957
R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049
R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635
R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.9489:R84329
R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083

R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens] //1.1e-101:528:95//Hs.22934:AA581379

R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916

R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873

R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064

R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777

R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080

R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823

R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847

R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839

R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592

R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans] //4.6e-70:348:96//Hs.11282:AI147040

R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247

R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089

R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus] //1.9e-77:364:100//Hs.12152:AA156214

R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans] //2.1e-101:558:93//Hs.18171:AA524327

R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600

R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236

R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans] //2.8e-16:93:100//Hs.107747:AI357868

R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295

R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344

R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs
.155464:AF088219
R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C
HAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333
R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161
R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033
R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547
R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING
XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911
R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//
Hs.61408:AF070621
R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930
R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF06
8179
R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788
R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187
R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659
R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5
e-48:276:81//Hs.72660:AB011157
R-HEMBA1003939
R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669
R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545
R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591
R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562
R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253
R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525
R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882
R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT

RY !!!! [H.sapiens]//2.2e-91:448:97//Hs.117834:AA766771
R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756
R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682
R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105
R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899
R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011
R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774
R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461
R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191
R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253
R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804
R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469
R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717
R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754
R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080
R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988
R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652
R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918
R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562
R-HEMBA1004133
R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736
R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320
R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs

.155464:AF088219

R-HEMBA1004150//GRANALCALIN//0.99:357:59//Hs.79381:M81637

R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087

R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855

R-HEMBA1004199

R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701

R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays] //1.7e-107:552:94//Hs.10092:AI189282

R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518

R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748

R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617

R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNIN G ENTRY !!!! [H.sapiens] //4.0e-16:117:91//Hs.92033:AA255832

R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353

R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389

R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258

R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus] //2.1e-61:221:86//Hs.7089:W37284

R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962

R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN G ENTRY !!!! [H.sapiens] //1.4e-89:465:95//Hs.113660:D20018

R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931

R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081

R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus] //4.4e-92:559:89//Hs.28298:AA203228

R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795

R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061

R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans] //3.6e-93:496:94//Hs.14337:AA534961

R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426

R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679

R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281

R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904

R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714

R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561

R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231

R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336

R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240

R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667

R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353

R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494

R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869

R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057

R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264

R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084

R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219

R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717

R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933

R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518

R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503

R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829

R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033

R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172

R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306

R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034

R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941

R-HEMBA1004507

R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271

R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947

R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972

R-HEMBA1004554

R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913

R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243

R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769

R-nnnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661
R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767
R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0501//4.6e-52:327:85//Hs.159897:AB007970
R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915
R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785
R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152
R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN RO
5D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12
263:AA282393
R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454
R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442
R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348
R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560
R-HEMBA1004672//EST//6.7e-76:315:97//Hs.20821:R19368
R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252
R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562
R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042
R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881
R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs
.155464:AF088219
R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235
R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequence//2.1e-44:467:73//
Hs.91916:AF035317
R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151
R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275
R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation
groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828
R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651

R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428
R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081
R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L0649
8
R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679
R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504
R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380
R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705
R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092
R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633
R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476
R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167
R-nnnnnnnnnnnnnnn
R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732
R-HEMBA1004806
R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676
R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784
R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:M74002
R-HEMBA1004847
R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120
R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267
R-HEMBA1004864
R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362
R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409
R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676
R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470
R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011

R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390

R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388

R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053

R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053

R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883

R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215

R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434

R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007

R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074

R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040

R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035

R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065

R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404

R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683

R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329

R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894

R-HEMBA1004995

R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520

R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548

R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM

OLOG [Homo sapiens] //8.4e-95:491:94//Hs.16085:AI261382
R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:8
5//Hs.22271:D26067
R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens] /
/2.6e-48:443:78//Hs.139019:N99348
R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Can
is familiaris] //1.2e-87:542:87//Hs.16258:AI376436
R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451
R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.7938
5:U90905
R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789
R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U
17077
R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete
cds//1.7e-111:545:96//Hs.11170:AF080561
R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739
R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952
R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85/
/Hs.19949:X98173
R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//4.7e-36:394:75//Hs.67619:AB007957
R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-3
2:362:77//Hs.132206:AF039694
R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397
R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914
R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766
R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239

R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) m
RNA, complete cds//0.84:191:61//Hs.26931:AF061836

R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284

R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687

R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331

R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834

R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896

R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1
e-49:277:93//Hs.72660:AB011157

R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862

R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391

R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750

R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs
.155464:AF088219

R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs
.32567:AF073519

R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046

R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169

R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472

R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83
733:X15606

R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467

R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
lete cds//4.7e-46:294:81//Hs.129735:AF010144

R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0
:210:62//Hs.4:X03350

R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653

R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305

R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.544
86:X54150

R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cdna yk3
0b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568

R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278

R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725

R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059

R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)
mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248

R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//
Hs.136309:AB007960

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//
/Hs.6445:L40391

R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961

R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494

R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:
85//Hs.153014:AB002353

R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
8.4e-73:464:87//Hs.103948:K00627

R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445

R-HEMBA1005497

R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788

R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis,
mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544

R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870

R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans
]//2.6e-82:387:99//Hs.67466:AI219740

R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322

R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045
 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:
 179:84//Hs.42674:U61981
 R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cer
 evisiae]//8.6e-115:578:95//Hs.17035:AI080471
 R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350
 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:
 439:91//Hs.22897:R43193
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103
 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497
 R-HEMBA1005577
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64
 //Hs.57929:AB011538
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392
 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539
 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820
 R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125
 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390
 R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422
 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisi
 ae]//2.8e-95:539:92//Hs.19400:AA662845
 R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:3

17:78//Hs.1721:X58377

R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081

R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522

R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.10458:AF088219

R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973

R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477

R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450

R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258

R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:U44060

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//1.7e-47:376:84//Hs.26988:U66406

R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055

R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943

R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP) //1.2e-45:398:79//Hs.155481:AJ006470

R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815

R-nnnnnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672

R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096

R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:U21936

R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974

R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.10458:AF088219

R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601

R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960
R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201
R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618
R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911
R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917
R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970
R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252
R-HEMBA1005894
R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686
R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363
R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.
5e-45:446:75//Hs.59403:AB011098
R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867
R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418
R-HEMBA1005963
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.26285:AF082516
R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45
:551:70//Hs.148495:AF050199
R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618
R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875
R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4
e-28:444:67//Hs.26450:AB018268
R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951
R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508
R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490
R-nnnnnnnnnnnnn

R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612
 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517
 R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313
 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA,
 complete cds//3.4e-43:328:82//Hs.73614:U83460
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293
 R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.
 7e-27:296:73//Hs.119387:AB007958
 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542
 R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212
 R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U3193
 0
 R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627
 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906
 R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97/
 /Hs.109268:AF070557
 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus m
 usculus] //3.3e-114:581:95//Hs.23617:AA928683
 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:7
 6//Hs.74554:D38522
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5
 .7e-30:179:91//Hs.15836:AF083384
 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84/
 /Hs.41742:AB007881
 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive

[M.musculus] //1.2e-97:529:93//Hs.10552:AA524401
R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE
[H.sapiens] //2.7e-88:484:92//Hs.104129:AA923278
R-nnnnnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770
R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDI
NG PROTEIN NAB2 [S.cerevisiae] //1.6e-66:377:91//Hs.108674:W25821
R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735
R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037
R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:16
7:86//Hs.74478:U33931
R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculu
s] //5.6e-76:417:94//Hs.111754:AI204587
R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs
.155464:AF088219
R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518
:U49184
R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//
Hs.79706:U53204
R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN
SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae] //3.6e-119:582:9
7//Hs.42343:AI417075
R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
R-HEMBA1006377//EST//0.0097:145:62//Hs.133027:AI049830
R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0
e-41:349:79//Hs.154872:AB011166
R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651

R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0
e-87:582:84//Hs.23094:M19503

R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:A1218923

R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778

R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878

R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13
:263:66//Hs.43127:AA258004

R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964

R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380

R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:
487:58//Hs.32963:D31784

R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895

R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-
17:342:63//Hs.111730:AA604403

R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441

R-HEMBA1006474

R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete
cds//4.2e-40:365:78//Hs.46468:U45984

R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.13
2243:Y07701

R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223

R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350

R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720

R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387

R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117

R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:
135:72//Hs.2161:M62505

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9

e-117:570:96//Hs.153858:AB014566
R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300
R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628
R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934
R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331
R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2
e-48:287:91//Hs.79507:AB011154
R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated
protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594
R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064
R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725
R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876
R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.
5e-29:276:76//Hs.144563:AF057280
R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390
R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs
.155464:AF088219
R-HEMBA1006612
R-HEMBA1006617//ESTs//1.2e-25:225:80//Hs.138852:AA284247
R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630
R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:9
0//Hs.22271:D26067
R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN
G ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889
R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [
Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185
R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete

cds//8.1e-108:567:94//Hs.6196:U40282
 R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427
 R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511
 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102
 R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594
 R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842
 R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435
 R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apar-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263
 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695
 R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens] //1.1e-92:483:94//Hs.6525:AI205313
 R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062
 R-HEMBA1006717
 R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099
 R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305
 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272

R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:8
 3//Hs.154326:D42087
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.
 8e-67:611:74//Hs.15519:AB018315
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:21
 3:84//Hs.9096:AA029400
 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein/
 /6.5e-77:371:98//Hs.42644:AJ010841
 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:3
 68:80//Hs.149323:AB002325
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-1
 12:558:96//Hs.107905:AI248363
 R-HEMBA1007045
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839

R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING
 ENTRY !!!! [H.sapiens]//7.2e-40:163:83//Hs.152369:AA504818
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121
 493:D25272
 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
 R-HEMBA1007147
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
 R-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:9
 4//Hs.22396:AF062085
 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.
 7e-62:332:95//Hs.3363:D86987
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4
 e-98:471:97//Hs.27197:AB018340
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83/
 /Hs.43681:AL022394
 R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207

R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
 R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804
 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
 R-HEMBA1007301
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens] //5.5e-15:311:64//Hs.142764:AA205569
 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684
 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
 R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens] //3.3e-44:341:71//Hs.111730:AA604403
 R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member L1 GHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090
 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969
 R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418
 R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332
 R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449
 R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C3 4E10.1 IN CHROMOSOME III [Caenorhabditis elegans] //6.0e-92:477:95//Hs.4877:AA418465
 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928

R-HEMBB1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702
 R-HEMBB1000044//EST//7.6e-70:367:95//Hs.140860:R42954
 R-HEMBB1000048//EST//1.5e-45:262:91//Hs.157627:AI357802
 R-HEMBB1000050//ESTs//0.039:91:74//Hs.163189:AA236903
 R-HEMBB1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107
 R-HEMBB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUC
 TASE COMPLEX SUBUNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//H
 s.116490:AA659584
 R-HEMBB1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939
 R-HEMBB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:
 80//Hs.4953:D63997
 R-HEMBB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:
 70//Hs.153014:AB002353
 R-HEMBB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
 R-HEMBB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5
 e-18:298:69//Hs.153026:AB014540
 R-HEMBB1000113//EST//8.2e-94:437:100//Hs.136893:AA805239
 R-HEMBB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521
 R-HEMBB1000136//ESTs//0.043:262:59//Hs.61304:AA025692
 R-HEMBB1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915
 R-HEMBB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
 R-HEMBB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
 R-HEMBB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558
 R-HEMBB1000198//ESTs//1.0:123:62//Hs.116602:AA665965
 R-HEMBB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:
 86//Hs.153014:AB002353
 R-HEMBB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364
 R-HEMBB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF
 F40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019

R-HEM BB1000226//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B04
95.8 IN CHROMOSOME II [C.elegans] //5.1e-73:449:89//Hs.16803:AA843214

R-HEM BB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106

R-HEM BB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs
.155464:AF088219

R-HEM BB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783

R-HEM BB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

R-HEM BB1000264

R-HEM BB1000266//ESTs, Weakly similar to similar to the beta transducin f
amily [C.elegans] //2.7e-102:556:93//Hs.16079:AA083522

R-HEM BB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385

R-HEM BB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9
e-24:198:72//Hs.101414:AB011129

R-HEM BB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458

R-HEM BB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:
87//Hs.153014:AB002353

R-HEM BB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601

R-HEM BB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034

R-HEM BB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs
.155464:AF088219

R-HEM BB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576

R-HEM BB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480

R-HEM BB1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084

R-HEM BB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs
.155464:AF088219

R-HEM BB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736

R-HEM BB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651

R-HEM BB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020

R-HEM BB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:

65//Hs.36232:D80008

R-HEM BB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590

R-HEM BB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//2.3e-56:335:77//Hs.92381:AB007956

R-HEM BB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.
66710:X96969

R-HEM BB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840

R-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8
e-109:531:97//Hs.16184:AJ001642

R-HEM BB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72/
/Hs.19949:X98173

R-HEM BB1000404//ESTs//0.088:298:59//Hs.61607:AA032026

R-HEM BB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591

R-HEM BB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:8
9//Hs.154326:D42087

R-HEM BB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !
!!! [H.sapiens]//0.30:214:63//Hs.142209:AA873303

R-HEM BB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990

R-HEM BB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221

R-HEM BB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438

R-HEM BB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396

R-HEM BB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:9
0//Hs.40100:AB002390

R-HEM BB1000487//EST//0.78:87:68//Hs.134601:AI081506

R-HEM BB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs
.155464:AF088219

R-HEM BB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:31
2:76//Hs.113283:AF018080

R-HEM BB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125

R-HEM BB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703
 R-HEM BB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
 R-HEM BB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
 R-HEM BB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099
 R-HEM BB1000550//EST//2.9e-11:113:79//Hs.161503:N68662
 R-HEM BB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288
 R-HEM BB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986
 R-HEM BB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258
 R-HEM BB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709
 R-HEM BB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618
 R-HEM BB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247
 R-HEM BB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895
 R-HEM BB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704
 R-HEM BB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391
 R-HEM BB1000598//Human antisecretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
 R-HEM BB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125
 R-HEM BB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249
 R-HEM BB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
 R-HEM BB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
 R-HEM BB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522
 R-HEM BB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582
 R-HEM BB1000643//ESTs//0.0049:191:62//Hs.55445:W31963
 R-HEM BB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100

R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
 R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988
 R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
 R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293
 R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
 R-nnnnnnnnnnnnn//Homo sapiens neuroanl mRNA, complete cds//6.5e-52:287:93
 //Hs.158300:AF040723
 R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs
 .155464:AF088219
 R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
 R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-
 50:245:99//Hs.111730:AA604403
 R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//
 Hs.10351:AB002306
 R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881
 R-HEMBB1000738//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121
 493:D25272
 R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925
 R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522
 R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445
 R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541
 R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771
 R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSOR//1.3e-37:193:75//Hs.73
 734:Z23091
 R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
 R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
 R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs
 .155464:AF088219
 R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447

R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.
.155464:AF088219
R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881
R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545
R-HEMBB1000840//ATPase, Na+/K+ transporting, beta 2 polypeptide//1.3e-43
:163:84//Hs.78854:AF007876
R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.
5e-41:367:78//Hs.129740:AB011137
R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1
.0e-41:483:73//Hs.2379:U23942
R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141
R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258
R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.1e-46:327:83//Hs.
51048:X68830
R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881
R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066
R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:3
67:73//Hs.149323:AB002325
R-HEMBB1000915//ESTs//0.00018:188:61//Hs.144847:AI222742
R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84/
/Hs.127649:AB007874
R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784
R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:35

0:91//Hs.49163:AA532881
 R-HEM BB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1
 e-84:546:86//Hs.23094:M19503
 R-HEM BB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354
 R-HEM BB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007
 R-HEM BB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
 R-HEM BB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
 R-HEM BB1000991//EST//0.99:58:72//Hs.100246:T23625
 R-HEM BB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482
 :70//Hs.154103:AF061258
 R-HEM BB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
 R-HEM BB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapie
 ns] //2.3e-25:339:71//Hs.129992:H58762
 R-HEM BB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214
 R-HEM BB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
 R-HEM BB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:30
 5:76//Hs.113283:AF018080
 R-HEM BB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
 R-HEM BB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
 R-HEM BB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
 R-HEM BB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107
 R-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.
 1e-87:497:91//Hs.15832:AB014518
 R-HEM BB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.
 2e-26:125:81//Hs.5737:AB007944
 R-HEM BB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
 R-HEM BB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
 R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:51
 2:97//Hs.12953:AF034803

R-HEM BB1001096//Human HsLIM15 mRNA for HsLim15, complete cds//1.2e-20:23
3:70//Hs.37181:D64108

R-HEM BB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:
82//Hs.153014:AB002353

R-HEM BB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:29
6:87//Hs.113283:AF018080

R-HEM BB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426

R-HEM BB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092

R-HEM BB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942

R-HEM BB1001126

R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subuni
t mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077

R-HEM BB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962

R-HEM BB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881

R-HEM BB1001151

R-HEM BB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197

R-HEM BB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878

R-nnnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162

R-HEM BB1001177

R-HEM BB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349

R-HEM BB1001199

R-HEM BB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183

R-HEM BB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549

R-HEM BB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573

R-HEM BB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8
2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti
body IA4))//3.1e-44:298:87//Hs.103458:X53795

R-HEM BB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817

R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus] //3.8e-80:400:96//Hs.71873:AA148213

R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560

R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236

R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987

R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268

R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970

R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087

R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412

R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans] //2.6e-104:515:97//Hs.16606:W81021

R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840

R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112

R-HEMBB1001302

R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627

R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627

R-HEMBB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873

R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754

R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens] //6.5e-61:313:96//Hs.43071:AA206222

R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365

R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639

R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470

R-HEMBB1001346

R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354
 R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721
 R-HEMBB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055
 R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:7
 2//Hs.154326:D42087
 R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617
 R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs
 .155464:AF088219
 R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205
 R-HEMBB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699
 R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970
 R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350
 R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:3
 65:58//Hs.389:X76342
 R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
 R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
 R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846
 R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
 R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201
 R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236
 R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
 R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
 R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78/
 /Hs.41742:AB007881
 R-HEMBB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:6
 1//Hs.13275:AI341468
 R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norve
 gicus]//0.80:53:83//Hs.26799:W74481

R-HEM BB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515

R-HEM BB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280

R-HEM BB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915

R-HEM BB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159

R-HEM BB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459

R-HEM BB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353

R-HEM BB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869

R-HEM BB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274

R-HEM BB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962

R-HEM BB1001564//EST//1.3e-35:141:81//Hs.162197:AA535216

R-HEM BB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329

R-HEM BB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944

R-HEM BB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219

R-HEM BB1001588//EST//8.3e-27:363:69//Hs.141603:N66015

R-HEM BB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184

R-HEM BB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044

R-HEM BB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888

R-HEM BB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272

R-HEM BB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082

R-HEM BB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633

R-HEM BB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813

R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438
 R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577
 R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572
 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.
 9e-117:573:97//Hs.24439:AB014546
 R-HEMBB1001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:
 523:97//Hs.26939:AA804534
 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358
 R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867
 R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038
 R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080
 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sa
 piens]//4.9e-32:277:73//Hs.142764:AA205569
 R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645
 R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO
 MOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113
 R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403
 R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488
 R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287
 R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059
 R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211
 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:
 74//Hs.70008:L00352
 R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369
 R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406
 R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253
 R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391
 R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247

R-HEM BB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503

R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI P1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209

R-HEM BB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0488//9.6e-39:288:73//Hs.67619:AB007957

R-HEM BB1001839

R-HEM BB1001850//EST//0.020:119:68//Hs.32767:H38125

R-HEM BB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539

R-HEM BB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106

R-HEM BB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397

R-HEM BB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434

R-HEM BB1001872//EST//0.85:156:64//Hs.119501:AA487980

R-HEM BB1001874//EST//0.64:107:70//Hs.147482:AI215572

R-HEM BB1001875//EST//0.079:199:59//Hs.121810:AA775240

R-HEM BB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081

R-HEM BB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310

R-HEM BB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191

R-HEM BB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725

R-HEM BB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915

R-HEM BB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216

R-HEM BB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750

R-HEM BB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897

R-HEM BB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390

R-HEM BB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531:70//Hs.153086:Y11251

R-HEM BB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:1
99:77//Hs.149323:AB002325

R-HEM BB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875

R-HEM BB1001944//EST//0.034:228:57//Hs.93664:N23366

R-HEM BB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875

R-HEM BB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589

R-HEM BB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998

R-HEM BB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:8
3//Hs.74554:D38522

R-HEM BB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881

R-HEM BB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972

R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.
3e-61:296:88//Hs.153468:AB011147

R-HEM BB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531

R-HEM BB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475

R-HEM BB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572

R-HEM BB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223

R-HEM BB1001996

R-HEM BB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798

R-HEM BB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
3.0e-18:222:71//Hs.103948:K00627

R-HEM BB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334

R-HEM BB1002009//EST//2.9e-44:245:94//Hs.28788:R66896

R-HEM BB1002015//EST//0.0027:198:63//Hs.160868:AI359052

R-HEM BB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900

R-HEM BB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426

R-HEM BB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638

R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:30

1:85//Hs.113283:AF018080
R-HEM BB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638
R-HEM BB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840
R-HEM BB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671
R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144
R-HEM BB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193
R-HEM BB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881
R-HEM BB1002115
R-HEM BB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814
R-HEM BB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006
R-HEM BB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553
R-HEM BB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073
R-HEM BB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185
R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934
R-HEM BB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881
R-HEM BB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841
R-HEM BB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584
R-HEM BB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631
R-HEM BB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807
R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503
R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363
R-HEM BB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112
R-HEM BB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223

R-HEMBB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305
 R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67/
 /Hs.155174:AB007892
 R-HEMBB1002327//EST//0.042:249:61//Hs.121097:AA714637
 R-HEMBB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312
 R-HEMBB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228
 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein/
 /0.85:46:84//Hs.42644:AJ010841
 R-HEMBB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322
 R-HEMBB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613
 R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:6
 5//Hs.74554:D38522
 R-HEMBB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085
 R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs
 .142296:AF072467
 R-HEMBB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055
 R-HEMBB1002387
 R-HEMBB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//2.3e-23:168:77//Hs.133526:N21103
 R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.
 2e-57:304:90//Hs.144563:AF057280
 R-HEMBB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293
 R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:
 87//Hs.153014:AB002353
 R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:7
 1//Hs.154326:D42087
 R-HEMBB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089
 R-HEMBB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083
 R-HEMBB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176

R-HEMBB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969
R-HEMBB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017
R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98/
/Hs.141515:T41142
R-HEMBB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615
R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.
2e-48:265:95//Hs.48827:AA873278
R-HEMBB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538
R-HEMBB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, comp
lete cds//0.50:142:69//Hs.159301:U43672
R-HEMBB1002531//EST//0.024:147:61//Hs.148305:AA909605
R-HEMBB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478
R-HEMBB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259
R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C
.elegans]//5.1e-22:210:81//Hs.11896:T68813
R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344:82//Hs.
51048:X68830
R-HEMBB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189
R-HEMBB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045
R-HEMBB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138
R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:8
7//Hs.154326:D42087
R-HEMBB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424
R-HEMBB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923
R-HEMBB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881
R-HEMBB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896
R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265
R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0508//8.5e-47:278:83//Hs.159187:AB007977
R-HEMBB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150
R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917
R-HEMBB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247
R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219
R-HEMBB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881
R-HEMBB1002677//ESTs//0.65:159:62//Hs.163517:AI419775
R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase //8.6e-54:543:75//Hs.2638:Z28339
R-HEMBB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646
R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753
R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099
R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487
R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398
R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842
R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547
R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682
R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701
R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219
R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304
R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165

R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350

R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531

R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065

R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099

R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241

R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713

R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352

R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172

R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577

R-MAMMA1000133

R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017

R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970

R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881

R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263

R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787

R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:AJ224162

R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069

R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611

R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054
R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881
R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.muscu
lus] //1.4e-41:272:90//Hs.68398:AA421103
R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946
R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.
3e-47:322:86//Hs.15519:AB018315
R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LI
GHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090
R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041
R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF0
10238
R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814
R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0508//2.7e-57:304:78//Hs.159187:AB007977
R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124
:AF019369
R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694
R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//3.1e-58:295:83//Hs.92381:AB007956
R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066
R-MAMMA1000287
R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.
155174:AB007892
R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:7
6//Hs.22271:D26067
R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251
R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434

R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491
R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]
//8.6e-54:278:97//Hs.139170:AA662998
R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881
R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.8
2:204:61//Hs.154919:AB014525
R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159
R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces
cerevisiae] //0.42:172:61//Hs.11463:AA535912
R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:8
2//Hs.154326:D42087
R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659
R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto
r, complete cds//8.6e-14:106:92//Hs.32170:AB015132
R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AI301060
R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLY
PROTEIN [Mus musculus] //9.1e-47:316:81//Hs.138698:N38973
R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198
R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.
3e-27:304:72//Hs.119387:AB007958
R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA,
complete cds//1.5e-58:282:82//Hs.97203:U83171
R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:8
1//Hs.40100:AB002390

R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452

R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461

R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171

R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179

R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447

R-MAMMA1000458

R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176

R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361

R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959

R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886

R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759

R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219

R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390

R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390

R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267

R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236

R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131

R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561

R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211

R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872

R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548

R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219

R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042

R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267

R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105

R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180

R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361

R-MAMMA1000623

R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002

R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203

R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162

R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3' REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065

R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476

R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212

R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343

R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644

R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333

R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569

R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515

R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329

R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942

R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267
R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893
R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1
098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141
429:AA631915
R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:2
53:98//Hs.31575:AF100141
R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis a
ntheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632
288
R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205
R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3
e-90:568:86//Hs.23094:M19503
R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627
R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131
R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256
R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:
76//Hs.153014:AB002353
R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204
R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439
R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150
R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73
919:X81637
R-MAMMA1000831//ESTs//1.3e-104:510:97//Hs.17494:AA572675
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902
R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358

R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097
 R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955
 R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251
 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390
 R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212
 R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311
 R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922
 R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099
 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399
 R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875
 R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243
 R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128
 R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166
 R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107
 R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215
 R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329
 R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093
 R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634
 R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989
 R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696
 R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335
 R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727
 R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281

R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428
R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducibl
e), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8
2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti
body IA4))//7.5e-49:340:85//Hs.103458:X53795
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.
0e-48:216:85//Hs.153468:AB011147.
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0
e-39:338:79//Hs.93121:AB018304
R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apa
f-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263
R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82/
/Hs.80738:X52075
R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:9
7//Hs.25863:AA630313
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86/
/Hs.153563:AF011333
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461
R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:9
1//Hs.40100:AB002390
R-nnnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650
R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881

R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus] //1
 .7e-13:273:65//Hs.98738:AI015487

R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532

R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748

R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:
 68//Hs.153014:AB002353

R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944

R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7
 e-84:556:85//Hs.23094:M19503

R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222

R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926

R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2
 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587

R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete c
 ds//4.2e-27:232:76//Hs.61840:U28686

R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576

R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
 3429 nt] //8.8e-53:462:78//Hs.116007:S79267

R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-5
 9:460:81//Hs.5247:AF029750

R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029

R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399

R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF06
 8179

R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131

R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-5
 8:409:84//Hs.5247:AF029750

R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus] //2.1e-91:430:
 99//Hs.129982:AI420970

R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959
R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202
R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637
R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148
R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307
R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561
R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643
R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144
R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.

2e-27:348:70//Hs.15731:AB011135
R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete
cds//4.0e-43:300:85//Hs.46468:U45984
R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, com
plete cds//8.8e-12:188:70//Hs.55771:AF004709
R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs
.32567:AF073519
R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322
R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881
R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831
R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, comp
lete cds//1.6e-19:117:96//Hs.19122:AF038957
R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267
R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168
R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618
R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67
//Hs.155174:AB007892
R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542
R-MAMMA1001465
R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) m
RNA, complete cds//0.79:182:66//Hs.136529:AF058317
R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78/

/Hs.43681:AL022394

R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065

R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522

R-MAMMA1001510

R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242

R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969

R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696

R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140

R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens] //1.9e-111:549:96//Hs.21635:AI417305

R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441

R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

R-MAMMA1001604

R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens] //1.9e-97:488:96//Hs.143263:AI057616

R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272

R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315

R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens] //6.8e-15:168:73//Hs.115216:AA291074

R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377

R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606

R-MAMMA1001649

R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp

lete cds//1.7e-54:272:81//Hs.129735:AF010144
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs
.155464:AF088219
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248
R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.0
66:196:62//Hs.159161:X69550
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//1.0e-17:246:73//Hs.67619:AB007957
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:
89//Hs.3094:D31884
R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088
R-MAMMA1001715//ESTs//1.2e-73:399:93//Hs.124620:AI082338
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus ga
llus]//3.7e-110:552:96//Hs.6923:AI161158
R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666
R-MAMMA1001744
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041
R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413
R-MAMMA1001757//ESTs//1.0e-98:488:96//Hs.45184:C14904
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276
R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:2
99:85//Hs.149323:AB002325
R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825
R-MAMMA1001771//ESTs, Moderately similar to semaphorin B [M.musculus]//7

.6e-43:257:91//Hs.7634:AA481246
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA,
complete cds//5.6e-42:272:86//Hs.73614:U83460
R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313
R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892
R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659
R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:
87//Hs.44106:D86979
R-MAMMA1001818
R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881
R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs
.32567:AF073519
R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83/
/Hs.43681:AL022394
R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811
R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461
R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs
.155464:AF088219
R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.
8e-31:262:77//Hs.5737:AB007944
R-nnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-0
6:450:58//Hs.132206:AF039694
R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA,
complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1
 .2e-46:429:78//Hs.2379:U23942

R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8
 2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti
 body IA4))//6.7e-47:283:89//Hs.103458:X53795

R-nnnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI251374

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.
 4e-18:174:77//Hs.139648:AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]
 //6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs
 .155464:AF088219

R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mR
 NA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs
 .32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete
 cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:78//Hs.138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//6.2e-51:318:82//Hs.92381:AB007956

R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2
e-45:283:88//Hs.153026:AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phos
phate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U486
96

R-MAMMA1002236

R-MAMMA1002243

R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:29
9:87//Hs.113283:AF018080

R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//1.6e-54:207:81//Hs.92381:AB007956

R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283

R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772

R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141

R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751

R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//
1.7e-39:203:81//Hs.154257:AI275982

R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881

R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454

R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153

R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO
MOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359

R-MAMMA1002308

R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mR
NA//2.2e-44:280:87//Hs.154069:U06452

R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3
e-70:503:81//Hs.23094:M19503
R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.
3e-49:457:76//Hs.144563:AF057280
R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183
R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084
R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//
Hs.91916:AF035317
R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897
R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618
R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439
R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-5
8:259:92//Hs.43628:Y15228
R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:7
7//Hs.40100:AB002390
R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367
R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73
919:X81637
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:48
3:84//Hs.113283:AF018080
R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475
R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2
(XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587
R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236
R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542
R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs

.155464:AF088219

R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061

R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845

R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294

R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488

R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588

R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477

R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475

R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348

R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996

R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.89121:AB007954

R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076

R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106

R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496

R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103

R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:AF055460

R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293

R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664

R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277
R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214
R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147
R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851
R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058
R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681
R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693
R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433
R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371
R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258
R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//Hs.1360:M29874
R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737
R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369
R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053
R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389
R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670
R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306
R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081
R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881
R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R. norvegicus]//2.3e-35:308:79//Hs.93332:AA811920
R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complet

e cds//9.7e-57:283:86//Hs.115325:D84488
R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:8
9//Hs.40100:AB002390
R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421
R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915
R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776
R-MAMMA1002655
R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75
//Hs.97476:AB007886
R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:8
2//Hs.154326:D42087
R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk5
2e10.5 [C.elegans]//5.3e-108:544:96//Hs.16464:W19606
R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.
6e-109:544:96//Hs.3363:D86987
R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385
R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675
R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510
R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//6.9e-70:353:96//Hs.138404:R70986
R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234
R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858
R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89/
/Hs.153563:AF011333
R-MAMMA1002727//ESTs//2.9e-84:395:100//Hs.162826:AA679571
R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs
.155464:AF088219
R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757

R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907
R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.154069:U06452
R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776
R-MAMMA1002758
R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281
R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651
R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272
R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750
R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145
R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812
R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198
R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260
R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319
R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881
R-MAMMA1002835
R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723
R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395
R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238
R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067
R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941
R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592
R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194
R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871
R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs

.155464:AF088219

R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811

R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEE
SB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783

R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:32
2:80//Hs.26929:AF008915

R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087

R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF06
8179

R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:7
6//Hs.90981:D80002

R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881

R-MAMMA1002938

R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1
e-83:556:85//Hs.23094:M19503

R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243

R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:
77//Hs.153014:AB002353

R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081

R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:5
25:95//Hs.94396:AA399630

R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835

R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279

R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF
F40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019

R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF06
8179

R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857

R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617

R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus] //1.4e-53:320:90//Hs.92023:AI022248

R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189

R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315

R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //3.5e-27:257:77//Hs.96337:AA225358

R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321

R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160

R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940

R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941

R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862

R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348

R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881

R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559

R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus] //1.1e-102:545:93//Hs.13755:AA878911

R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969

R-MAMMA1003089//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] //1.4e-34:421:70//Hs.161959:AA493652

R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651

R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283

R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366

R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788

R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125

R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537

R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861

R-nnnnnnnnnnnnnnn

R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster] //2.0e-87:524:89//Hs.6884:W30736

R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94/
/Hs.108112:AF070640

R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312

R-NT2RM4000027

R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663

R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI186169

R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379

R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e
-113:549:97//Hs.95665:AF070639

R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817

R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708

R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312

R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CY
TOPLASMIC [H.sapiens] //1.9e-99:536:92//Hs.127810:AI246301

R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397

R-nnnnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962

R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160

R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens] //4.1e-99
:542:93//Hs.6366:AA614113

R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723

R-NT2RM4000199//ESTs//0.020:95:65//Hs.146203:AI254528

R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876

R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs
.155464:AF088219

R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.
7e-103:546:94//Hs.111138:AB018255

R-NT2RM4000215

R-nnnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760

R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602

R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031

R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974

R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128

R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673

R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219

R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637

R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-117:579:96//Hs.5216:AA534881

R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:AI224479

R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063

R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542

R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140

R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:AA775879

R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977

R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285

R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.eleg

ans] //5.4e-75:470:90//Hs.69235:AA192359

R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173

R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:AI150687

R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865

R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae] //6.0e-99:492:96//Hs.21090:AA418587

R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens] //2.2e-102:493:97//Hs.111279:W84558

R-NT2RM4000496

R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:AI358465

R-NT2RM4000514//ESTs//1.7e-112:552:96//Hs.6686:AA205496

R-nnnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae] //1.4e-60:343:93//Hs.16014:AA074879

R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731

R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461

R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777

R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198

R-NT2RM4000585//EST//0.28:63:77//Hs.150024:AI291981

R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437

R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891

R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589

R-nnnnnnnnnnnnn//ESTs//1.5e-89:431:97//Hs.26117:W16697

R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli] //1.4e-102:519:96//Hs.14779:N64822

R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144

R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans] //2.9e-115:55

0:98//Hs.11820:AA205531
R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510
R-aaaaaaaaaaaaa
R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128
R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR
ECURSOR [Mus musculus] //2.2e-103:519:95//Hs.6823:W18181
R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6
e-105:536:95//Hs.137168:AB018303
R-NT2RM4000741//ESTs//0.99:266:58//Hs.142718:AA034046
R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988
R-NT2RM4000764
R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.
3e-106:546:94//Hs.18586:AB007920
R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mR
NA//6.5e-40:424:73//Hs.154069:U06452
R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:AI417008
R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//
Hs.20991:D31891
R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3'
end//2.5e-28:158:96//Hs.118249:M21868
R-NT2RM4000813
R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]
//1.3e-109:539:97//Hs.99636:AI219667
R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-11
2:448:99//Hs.20223:AA482031
R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864

R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343
R-aaaaaaaaaaaaaaaa
R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNIN
G ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514
R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887
R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647
R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien
s]//1.7e-82:414:96//Hs.115342:AA650126
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8
e-114:545:97//Hs.19542:AB018272
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5
e-114:556:97//Hs.15711:AB014539
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352
R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto
r, complete cds//0.42:133:67//Hs.32170:AB015132
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300
R-aaaaaaaaaaaaaaaa//ESTs//3.4e-91:439:99//Hs.103177:W72798
R-NT2RM4001092//ESTs//1.4e-86:517:89//Hs.132969:Z78324
R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848
R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085
R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
G ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3
.1e-32:274:70//Hs.2379:U23942

R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849
 R-NT2RM4001203
 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307
 R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410
 R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677
 R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184
 R-NT2RM4001309
 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857
 R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899
 R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352
 R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae] //1.9e-105:522:97//Hs.18442:AI129307
 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339
 R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476
 R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211
 R-NT2RM4001382
 R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507
 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790
 R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus] //4.0e-102:539:94//Hs.15744:AI055859
 R-NT2RM4001412
 R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895
 R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054
 R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae] //7.4e-108:544:94//Hs.7558:AA526812
 R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277
 R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739
 R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067

R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.
0e-104:547:93//Hs.153121:AB014585

R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664

R-NT2RM4001522//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.
.155464:AF088219

R-NT2RM4001557//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:16
5:83//Hs.29134:H43072

R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027

R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-
11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a
alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6
-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. C
ontains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z
98046

R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009

R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946

R-nnnnnnnnnnnnnnn

R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171

R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.
1e-112:565:95//Hs.23255:AB018334

R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079

R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957

R-NT2RM4001650

R-NT2RM4001662

R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.
6e-36:230:70//Hs.7764:AB007938

R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496

R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440

R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686
R-nnnnnnnnnnnnn//ESTs//6.5e-104:487:99//Hs.153581:AA630465
R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans] //3.1e-108:563:94//Hs.18510:AA522887
R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt] //0.083:124:68//Hs.120980:S83390
R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200
R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629
R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270
R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956
R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567
R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920
R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839
R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551
R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070
R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619
R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] //4.1e-10:274:62//Hs.161959:AA493652
R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans] //3.0e-43:292:86//Hs.14202:N46000
R-nnnnnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280
R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711
R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252
R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149
R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178

R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens] //1.2e-105:535:95//Hs.30991:AA994438

R-NT2RM4001930//ESTs//4.1e-84:425:96//Hs.80042:N63143

R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893

R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-1
10:556:95//Hs.118631:AF098162

R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268

R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]
//5.7e-62:326:95//Hs.3385:N25917

R-nnnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9
e-21:121:98//Hs.8772:AA521097

R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265

R-NT2RM4001984

R-NT2RM4001987

R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528

R-NT2RM4002018

R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:8
7//Hs.154326:D42087

R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435

R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226

R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887

R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF06
8179

R-nnnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//
5.5e-42:554:68//Hs.85313:AF071309

R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
2.3e-43:468:73//Hs.139107:K00629

R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthet
ase [H.sapiens] //6.8e-57:290:96//Hs.109274:AA193416

R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655
R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528
R-nnnnnnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409
R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:
Y13620
R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712
R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987
R-NT2RM4002146//ESTs//1.9e-93:439:99//Hs.119295:AA442090
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111
:560:96//Hs.22464:AF084535
R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552
:72//Hs.154103:AF061258
R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400
R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343
R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678
R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079
R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUN
D [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984
R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-gl
ycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-1
00:544:93//Hs.27567:W72190
R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs
.155464:AF088219
R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864
R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263
R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638
R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461
R-NT2RM4002294
R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164

R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498
R-nnnnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913
R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:
66//Hs.155129:M77198
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.
8e-122:593:97//Hs.26163:AB014549
R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594
R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884
R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328
R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk5
2e10.5 [C.elegans]//1.3e-97:473:98//Hs.16464:W19606
R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677
R-NT2RM4002446
R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142
R-NT2RM4002457
R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete
cds//1.6e-103:507:97//Hs.8765:AF083255
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.
3e-32:172:98//Hs.94781:AB014591
R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884
R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029
R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464
R-nnnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 re
ceptor [H.sapiens]//1.4e-73:360:91//Hs.31030:H50467
R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788
R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057
R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312
R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYLGALACTOSAMI

NYLTRANSFERASE [Bos taurus] //2.3e-89:435:97//Hs.15830:AA165698
 R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569
 R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermu
 s aquaticus thermophilus] //9.6e-28:194:87//Hs.59346:AI126802
 R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096
 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081
 R-NT2RP2000008//Zinc finger protein 37a (K0X 21)//5.2e-25:366:67//Hs.544
 88:X69115
 R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713
 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7
 e-42:223:96//Hs.8309:AB018290
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol
 og (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749
 R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798
 R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910
 R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanog
 aster] //2.3e-35:199:94//Hs.41793:AA775879
 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//
 /1.4e-78:383:98//Hs.58254:W72881
 R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097
 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA; com
 plete cds//1.1e-78:379:97//Hs.54877:AF050078
 R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcr
 ipt, partial//2.9e-21:232:75//Hs.102576:AJ010230
 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8
 e-75:378:96//Hs.22926:AB018338
 R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236
 :63//Hs.41:D90064
 R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757

R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827
R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419
R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-7
6:386:95//Hs.17706:AB018356
R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK7
57.1 IN CHROMOSOME III [C.elegans]//1.9e-19:153:86//Hs.5268:W22670
R-nnnnnnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099
R-nnnnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513
R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN
AP47 [Mus musculus]//3.0e-89:457:95//Hs.3832:AI208601
R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548
R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820
R-NT2RP2000161//ESTs//1.6e-99:492:97//Hs.21738:AI188190
R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741
R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373
R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510
R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897
R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94/
/Hs.79402:AC004382
R-NT2RP2000232
R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683
R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379
R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.s
apiens]//1.3e-95:454:99//Hs.102057:AA649005
R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840
R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649
R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM
OLOG [Homosapiens]//8.4e-59:298:96//Hs.16085:AI261382

R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635
R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865
R-NT2RP2000289
R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.
8e-106:494:99//Hs.102951:AA574249
R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712
R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA
, complete cds//2.8e-39:222:93//Hs.58218:U82381
R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome
1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehyd
rogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF
6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contain
s ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398
R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITO
CHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441
R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062
R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA,
complete cds//1.1e-47:262:94//Hs.76556:U83981
R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103
R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09
:93:83//Hs.808:L28010
R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
complete cds//4.2e-20:140:90//Hs.5819:AF102265
R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65
:362:93//Hs.22197:AI151425
R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN
PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:9
2//Hs.21938:W81045

R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013
R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078
R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215
R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.
.110:AB007896
R-nnnnnnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348
R-NT2RP2000523
R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5
e-30:167:97//Hs.14409:AB011144
R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1
e-66:335:96//Hs.7314:AB014514
R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222
R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275
R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396
R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767
R-NT2RP2000678//ESTs//2.6e-53:271:96//Hs.23790:N99347
R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368
R-NT2RP2000715//EST//1.2e-87:418:99//Hs.139425:AA429279
R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965
R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:N62642
R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419
R-NT2RP2000809
R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745
R-nnnnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404
R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918
R-NT2RP2000819
R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511
R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR/

/4.6e-10:247:66//Hs.29352:M31165
R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552
R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345
R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:AB018284
R-NT2RP2000892//ESTs//2.8e-50:258:96//Hs.119238:AA476267
R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266
R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:AB018298
R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021
R-NT2RP2000970//EST//8.7e-06:255:62//Hs.149202:AI246481
R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537
R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521
R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643
R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660
R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108
R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665
R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068
R-NT2RP2001119
R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348
R-NT2RP2001137
R-NT2RP2001149//ESTs//5.1e-66:324:97//Hs.27475:AA704512
R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145

R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:AB007949

R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287

R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510

R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402

R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358

R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//Hs.44014:AA632298

R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353

R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229

R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775

R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665

R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205

R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//2.3e-43:238:93//Hs.106632:N25679

R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138

R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178

R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028

R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038

R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]//3.9e-74:411:93//Hs.47305:AA195153

R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875

R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:469:97//Hs.20483:AA522505

R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030

R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

R-NT2RP2001427//EST//1.7e-11:107:84//Hs.148584:AI201728

R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:55
8:97//Hs.7627:AI341556

R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394

R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453

R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765

R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539

R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs
.155464:AF088219

R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513

R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146

R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL
AR1//6.7e-106:545:95//Hs.4277:Y14494

R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240

R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3
(XRCC3) mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586

R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816

R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//2.0e-76:387:96//Hs.67619:AB007957

R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60/
/Hs.119:D14661

R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884

R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995

R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767

R-NT2RP2001613

R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294

R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090

R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845

R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336

R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323

R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579
 R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538
 R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100
 R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EX01a) mRNA, complete cds//
 2.1e-105:519:96//Hs.47504:AF091754
 R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037
 R-NT2RP2001861
 R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941
 R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088
 R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //6.9e-110:556:95//Hs.23159:AA113849
 R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724
 R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423
 R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268
 R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087
 R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180
 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594
 R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588
 R-NT2RP2001969
 R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1
 [M.musculus] //8.3e-15:118:89//Hs.18760:AA166678
 R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233
 R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332
 R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627
 R-NT2RP2002041
 R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938
 R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895

R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068
 R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091
 R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265
 R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:87//
 Hs.11039:AF052183
 R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524
 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e
 -60:376:89//Hs.155218:AJ007509
 R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000
 R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134
 R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527
 R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268
 R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495
 R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:26
 9:98//Hs.107201:W52859
 R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//3.9e-15:245:71//Hs.87578:AI125363
 R-NT2RP2002193//ESTs//3.5e-79:453:90//Hs.76578:AI290672
 R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946
 R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499
 R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341
 R-ntnnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus
]//5.4e-48:238:99//Hs.22583:AA188168
 R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cd
 s//1.6e-15:131:83//Hs.150595:AF005418
 R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//
 Hs.92137:M19720
 R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-1
 00:550:91//Hs.4029:Z78373

R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans] //3.2e-92:48
2:93//Hs.5570:AI377863

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,
partial cds//4.1e-103:527:94//Hs.24812:AF069532

R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015

R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA
, complete cds//1.2e-112:567:95//Hs.31034:AB015594

R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372

R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant m
RNA, complete cds//1.2e-103:600:89//Hs.109051:AF038958

R-NT2RP2002394//ESTs//0.11:158:65//Hs.28792:AI343467

R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815

R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.
7e-33:285:80//Hs.15731:AB011135

R-NT2RP2002439//ESTs//3.2e-12:134:76//Hs.32246:AA464020

R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521

R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230

R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233

R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complet
e cds//9.9e-115:605:92//Hs.125856:AB005289

R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180

R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.
5e-107:583:91//Hs.23255:AB018334

R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305

R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-10
9:570:93//Hs.49476:AF009314

R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325

R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien
s] //7.5e-118:564:97//Hs.94549:AA149547

R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783

R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170

R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220

R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615

R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881

R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

R-NT2RP2002672

R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB
//0.99:184:63//Hs.50727:U43572

R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223

R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210

R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626

R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300

R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.6
6:360:59//Hs.119139:AB011108

R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352

R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131

R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042

R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124

R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//
Hs.17481:AF070537

R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124

R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens] //1.6e-100:501:97//Hs.136202:AA206578

R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031

R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870

R-NT2RP2002880
 R-NT2RP2002891
 R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894
 R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143
 R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096
 R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771
 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480
 R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060
 R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213
 R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [*Drosophila melanogaster*] //3.1e-119:578:97//Hs.106290:AI125291
 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329
 R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [*H.sapiens*] //2.4e-98:467:98//Hs.86337:AA149311
 R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642
 R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594
 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082
 R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081
 R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512
 R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345
 R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355
 R-NT2RP2003125
 R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986
 R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506
 R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379
 R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067

R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952
 R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156
 R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816
 R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074
 R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253
 R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661
 R-NT2RP2003243//ESTs//3.6e-53:300:92//Hs.118793:AA192438
 R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937
 R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859
 R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:AB014525
 R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427
 R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106
 R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087
 R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321
 R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874
 R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126
 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948
 R-NT2RP2003339//ESTs//1.3e-85:441:96//Hs.24115:N32618
 R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825
 R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014
 R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476
 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502
 R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249

R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683

R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:AI016073

R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360

R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903.

R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332

R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121

R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:R52777

R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831

R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733

R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270

R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783

R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170

R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101

R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684

R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439

R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696

R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719

R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:AA126463

R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067

R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981
R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN
MURZ-RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188
R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951
R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523
R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62/
/Hs.65539:AI148540
R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.
norvegicus]//4.3e-99:492:96//Hs.93332:AA811920
R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246
R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4
e-47:265:93//Hs.78494:AB011097
R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401
R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003
R-ntnnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//
Hs.2384:U18914
R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2
-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W74577
R-NT2RP2003751
R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808
R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709
R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606
R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds/
/6.0e-106:531:96//Hs.90436:AF047437
R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811
R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836
R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955
R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077
R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838

R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124
R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167
R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341
R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611
R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.75875:U49278
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//Hs.35086:AB014458
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:AB007916
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347
R-NT2RP2003984
R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087
R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:AI149968
R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478
R-NT2RP2004041
R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706
R-NNNNNNNNNNNN//ESTs//1.4e-110:559:96//Hs.71916:AA219699
R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204
R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461
R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036
R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500
R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241
R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Ant hocidaris crassispina]//1.0e-118:583:97//Hs.16520:AI224533
R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544
R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974

R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589
 R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167
 R-NT2RP2004196
 R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756
 R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972
 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens] /
 /5.2e-105:499:98//Hs.143460:AA483305
 R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cd
 s//3.4e-103:530:93//Hs.54900:AF039687
 R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483
 R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744
 R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187
 R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete c
 ds//4.7e-110:544:96//Hs.61152:AF000416
 R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788
 R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223
 R-NT2RP2004347
 R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173
 R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310
 R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI218624
 R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192
 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN FO
 9G8.3 IN CHROMOSOME III [Caenorhabditis elegans] //1.4e-11:108:82//Hs.304
 90:AA146916
 R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646
 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473
 R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900

R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921
R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121
R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124
R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695
R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase
-1 (PDK1) mRNA, complete cds//8.6e-34:143:98//Hs.154729:AF017995
R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700
R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320
R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081
R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347
R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470
R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661
R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126
R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666
R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862
R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//4.5e-07:149:76//Hs.12845:N28835
R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497
R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587
:96//Hs.5198:AJ006291
R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9
e-107:520:96//Hs.29956:AB007929
R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930
R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858
R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0
e-120:600:96//Hs.154919:AB014525
R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:AI149793
R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433
R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.

3e-118:594:96//Hs.4236:AB007947

R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015

R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423

R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774

R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013

R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//8.0e-116:564:96//Hs.40820:AF058953

R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579

R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:AF054179

R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906

R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803

R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567

R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529

R-ntnnnnnnnnnnnnnn//ESTs//0.059:137:64//Hs.144109:AI345543

R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941

R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458

R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087

R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496

R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910

R-NT2RP2004985

R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902

R-NT2RP2005000

R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:AB014515

R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235

R-ntnnnnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161
 R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507
 R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887
 R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220
 R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757
 R-NT2RP2005108
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7
 e-105:518:97//Hs.22616:AB014564
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box
 protein)//4.6e-69:464:85//Hs.100555:X98743
 R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383
 R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180:AI341261
 R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744
 R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438
 R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582
 R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648
 R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//2.4e
 -101:513:95//Hs.155218:AJ007509
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 H
 OMOLOG [H.sapiens]//1.9e-115:577:96//Hs.7600:H98166
 R-NT2RP2005227//Homo sapiens LIM protein mRNA, complete cds//1.0e-45:359
 :82//Hs.154103:AF061258
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Sacc
 haromyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587
 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503
 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK
 637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.230
 47:N66596
 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272

R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219
R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590
R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261
R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338
R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701
R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699
R-NT2RP2005344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445
R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544
R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247
R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304
R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae] //2.5e-75:461:88//Hs.70849:AA121697
R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans] //8.1e-96:491:95//Hs.7194:AI185631
R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068
R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423
R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096
R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307
R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936
R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019
R-NT2RP2005476//ESTs//5.1e-40:205:98//Hs.101577:AI168526
R-NT2RP2005490//ESTs//1.3e-70:364:96//Hs.134382:AA083573
R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455

R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540
R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426
R-NT2RP2005498//ESTs, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD
REGULATORY SUBUNIT, NEURONAL ISOFORM [*Oryctolagus cuniculus*]//2.3e-45:2
84:88//Hs.85752:AI138993
R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755
R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C1
2C2.09C IN CHROMOSOME I [*Schizosaccharomyces pombe*]//8.2e-36:215:92//Hs.
5298:AA725071
R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA,
complete cds//3.2e-110:570:94//Hs.119023:AF092563
R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING EN
TRY !!!! [H.sapiens]//1.3e-84:433:95//Hs.36942:AA524535
R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856
R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e
-108:560:94//Hs.159597:AJ012449
R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.
7e-115:583:96//Hs.62515:AB007963
R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572
R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567
R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169
R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240
R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733
R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060
R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788
R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229
R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211
R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740
R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173

R-NT2RP2005651//ESTs, Highly similar to XFIN PROTEIN [Xenopus laevis] //
2.9e-103:525:96//Hs.70589:AA868470

R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:6
0//Hs.162:X16302

R-NT2RP2005669//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//2.7e
-14:87:100//Hs.146406:AF069987

R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, co
mplete cds//5.8e-91:434:98//Hs.25664:AF089814

R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229

R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236

R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643

R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tau
rus] //2.8e-68:376:93//Hs.9095:AA532630

R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3
e-105:503:98//Hs.61638:AB018342

R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precu
sor [H.sapiens] //5.4e-105:500:98//Hs.14298:AI417523

R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982

R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455

R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153

R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258

R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064

R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, c
omplete cds//4.3e-42:223:96//Hs.159651:AF068868

R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, comple
te cds//1.2e-104:494:98//Hs.26285:AF082516

R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163

R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463

R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTA

SE [Homo sapiens] //5.4e-112:559:96//Hs.14214:AI189379
R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa] //3.0e-108:544:96//Hs.22151:AI214321
R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664
R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724
R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398
R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746
R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981
R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122
R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403
R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062
R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462
R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105
R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133
R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315
R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268
R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans] //2.4e-73:397:94//Hs.16667:T92427
R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus] //2.8e-114:560:97//Hs.9082:AA873170
R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419
R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988
R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080
R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347
R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans] //1.2e-50:278:94//Hs.7194:AI185631
R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492
R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714

R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093
 R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA
 , complete cds//0.031:254:62//Hs.46440:U21943
 R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365
 R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255
 :72//Hs.154103:AF061258
 R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1
 e-110:553:95//Hs.109299:AB014554
 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.15129
 3:U79276
 R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398
 R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153
 910:X96484
 R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312
 R-NT2RP2006238//ESTs, Highly similar to ra8 [R.norvegicus]//1.5e-29:183:
 91//Hs.4048:AA404253
 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928
 R-NT2RP2006261//ESTs//3.4e-57:326:92//Hs.22523:W02999
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:4
 81:97//Hs.3404:AF035262
 R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapien
 s]//1.9e-89:460:96//Hs.21889:N78664
 R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771
 R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412
 R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321

R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411
R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducibl
e), polypeptide 2//3.9e-48:403:77//Hs.1361:M55053
R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complet
e cds//1.4e-27:155:76//Hs.115325:D84488
R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092
R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146
R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595
R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs
.72160:AJ006266
R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478
R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679
R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947
R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474
R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886
R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622
R-nnnnnnnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:AI393829
R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting
protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112
R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598
R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (J
M21)//1.9e-116:560:97//Hs.6764:AJ011972
R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs
.155464:AF088219
R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213
R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-
41:249:90//Hs.156155:AI222202
R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095
R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574

R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029
 R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715
 R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241
 R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2
 e-116:578:96//Hs.13273:AB011164
 R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418
 R-NT2RP3000186
 R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882
 R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091
 R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306
 R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817
 R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819
 R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239
 R-NT2RP3000251
 R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:
 532:97//Hs.111086:AI379177
 R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073
 R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446
 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sa
 piens]//3.6e-103:516:96//Hs.4894:AI191323
 R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117
 R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438
 R-NT2RP3000324
 R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267
 R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689
 R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225
 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:
 556:96//Hs.111086:AI379177

R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741
 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S
 .cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423
 R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303
 R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cd
 s//4.2e-111:529:98//Hs.28307:AF071185
 R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947
 R-NT2RP3000433
 R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340
 R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254
 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102
 R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492
 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragm
 ent//1.8e-23:347:70//Hs.114963:L34408
 R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600
 R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141
 R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667
 R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151
 R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161
 R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.
 95:85:71//Hs.5184:AA709151
 R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180
 R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI198036
 R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68/
 /Hs.79077:D87071
 R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447
 R-NT2RP3000582//ESTs//2.1e-25:131:80//Hs.152465:AA563785
 R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI241511

R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817
R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI190916
R-nnnnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:5
8//Hs.155045:AB002312
R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880
R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049
R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394
R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:5
45:98//Hs.4857:AI090739
R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.
3e-49:397:80//Hs.15519:AB018315
R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin c
arrier protein [H.sapiens]//6.3e-92:434:99//Hs.152517:AA719022
R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084
R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185
R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185
R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873
R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.146589:AI085578
R-NT2RP3000736
R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISP
HOSPHATE PHOSPHODIESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//
Hs.136065:W21960
R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:AI310447
R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243
R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI378583
R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810
R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582
R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081
R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082

R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022
 R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:AI051657
 R-NT2RP3000850
 R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272
 R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895
 R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741
 R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837
 R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI014673
 R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468
 R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217
 R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385
 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus] /
 /9.5e-113:566:96//Hs.5900:AA035728
 R-NT2RP3000919
 R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.5e-25:375:71//Hs.2953:X844
 07
 R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178
 R-NT2RP3000994//ESTs//3.5e-111:537:97//Hs.21146:AA683542
 R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405
 R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029
 R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044
 R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo
 sapiens] //5.6e-102:486:99//Hs.145956:AA007349
 R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)//0.00
 12:447:58//Hs.2133:U18991
 R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874
 R-NT2RP3001096//ESTs//1.1e-110:540:96//Hs.42824:AA873182
 R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832
 R-nnnnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325

R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster] //3.2e-104:543:95//Hs.93796:C06063

R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575

R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878

R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779

R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180

R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166

R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188

R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761

R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305

R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //9.6e-113:552:97//Hs.23900:U82984

R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717

R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266

R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460

R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139

R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963

R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196

R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399

R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens] //2.8e-89:462:95//Hs.116793:AA779588

R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus] //5.2e-82:466:91//Hs.66048:AA524416

R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631

R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997

R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135

R-NT2RP3001268//Human Aac11 (aac11) mRNA, complete cds//0.12:494:59//Hs.

151031:U83857

R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965

R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.113184:N25651

R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332

R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691

R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571

R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989

R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete
cds//0.22:199:63//Hs.159534:U35234

R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.
9e-114:566:96//Hs.18586:AB007920

R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653

R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798

R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090

R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778

R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP
95 [R.norvegicus]//5.7e-92:522:90//Hs.96200:AA218942

R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375

R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232

R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628

R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186

R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898

R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817

R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94/
/Hs.6957:AF052158

R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692

R-nnnnnnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:
533:91//Hs.85844:X66397

R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374

R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//5.1e-101:482:98//Hs.124135:AA910560

R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994

R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs
.155464:AF088219

R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA644658

R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280

R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009

R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783

R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-
61:338:93//Hs.519:U13395

R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (T
RC8) mRNA, complete cds//6.8e-112:549:97//Hs.28285:AF064801

R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047

R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-5
9:427:83//Hs.5247:AF029750

R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463

R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus
]//2.8e-76:392:95//Hs.66048:AA524416

R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477

R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:8
6:88//Hs.4311:AB015337

R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194

R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328

R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798

R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598

R-NT2RP3001629

R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:
541:96//Hs.9899:AF099149

R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989
R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189
R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225
R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558
R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312
R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669
R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//4.1e-80:444:91//Hs.6823:W18181
R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099
R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440
R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H. sapiens]//1.2e-87:450:96//Hs.20281:N92517
R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:AB007928
R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900
R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962
R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292

R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900
R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792
R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]
]//1.0e-40:202:100//Hs.24709:AI123300
R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781
R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737
R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1
[Saccharomyces cerevisiae]//1.3e-95:483:96//Hs.5771:W74591
R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990
R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325
R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889
R-NT2RP3001989//ESTs, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310
:99//Hs.11449:AI201540
R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088
R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087
:X86779
R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729
R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs
.155464:AF088219
R-NT2RP3002033
R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081
R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426
R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:AI365221
R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66/
/Hs.90438:D63486

R-NT2RP3002062

R-nnnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657

R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139

R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148

R-NT2RP3002102

R-NT2RP3002108

R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385

R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:AI249703

R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEI

N 1 HOMOLOG [Homo sapiens] //6.2e-107:534:96//Hs.59523:AA602837

R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293

R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024

R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713

R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120

R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI193598

R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446

R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588

R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672

R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743

R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171

R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898

R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500

R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN

1 HOMOLOG [H.sapiens]//1.8e-19:136:87//Hs.106928:AI041737

R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667

R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0

048:221:64//Hs.556:L41887

R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A)

gene//5.8e-105:516:94//Hs.6483:Y16355

R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:95//Hs.12707:AB014578

R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:71//Hs.28914:Y00486

R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185

R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526:90//Hs.8083:AA521436

R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246

R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272

R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673

R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184:63//Hs.89230:AF031815

R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129883:AB007880

R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850

R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673

R-NT2RP3002603

R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365

R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573

R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172

R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109:537:97//Hs.19348:AA151678

R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502

R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871

R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens] //5.0e-101:524:95//Hs.32580:AI123601
R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169
R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945
R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159
R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973
R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958
R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377
R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240
R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080
R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678
R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641
R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262
R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2
(XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587
R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5
e-110:570:95//Hs.6162:AB018314
R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286
R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975
R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698
R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0492//0.23:563:56//Hs.127338:AB007961
R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGAS
E 1 [Saccharomyces cerevisiae] //2.0e-56:387:86//Hs.144597:W20143
R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850
R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116
R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553
R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423
R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTE

IN [Mus musculus] //3.0e-100:528:94//Hs.90353:N98551
R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355
R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912
R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans] //5.9e-83:392:9
9//Hs.101364:AA534439
R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809
R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466
R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441
R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520
R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982
R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus
musculus] //3.3e-107:535:96//Hs.27437:AA004208
R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632
R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774
R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007
R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226
R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944
R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796
R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634
R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573
R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107
R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoide
um] //2.0e-40:229:93//Hs.17377:AI078151
R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343
R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628
R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960
R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061
R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:
550:93//Hs.11702:L36983

R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035
 R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055
 R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818
 R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261
 R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931
 R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445
 R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289
 R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993
 R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102
 R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155
 R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567
 R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272
 R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM
 OLOG [H.sapiens] //2.2e-24:418:67//Hs.139488:AI124095
 R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372
 R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041
 R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023
 R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete c
 ds//3.6e-97:479:96//Hs.14934:AF004828
 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1
 e-102:527:93//Hs.26450:AB018268
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //4.0e-106:549:94//Hs.7886:AI057529
 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U025
 56
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRN
 A//4.1e-33:217:88//Hs.8068:U00952

R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430
 R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681
 R-NT2RP3003564
 R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721
 R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944
 R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759
 R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448
 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//
 Hs.17217:U49957
 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310
 R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714
 R-NT2RP3003672
 R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036
 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768
 R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.
 6e-103:492:97//Hs.48513:AB018300
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863
 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913
 R-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC//8.9e-108:551
 :95//Hs.115742:AF077754
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446
 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidoca
 ldarius]//3.4e-89:456:95//Hs.5555:AI285198
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761
 R-NT2RP3003828//ESTs, Weakly similar to unknown [H.sapiens]//9.6e-98:511
 :95//Hs.26955:AI333224

R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611
 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962
 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298
 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170
 R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726
 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933
 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221
 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409
 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593
 R-NT2RP3004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142
 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714
 R-NT2RP3004041
 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820
 R-NT2RP3004070//ESTs//5.5e-108:552:95//Hs.23392:AI310139
 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W45387
 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104
 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402:95//Hs.55847:W31092
 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696
 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334
 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425
 R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200:100//Hs.26089:AA195126
 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41

:266:89//Hs.6314:AA522619

R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe] //3.7e-112:547:97//Hs.99819:AI346680

R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794

R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252

R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827

R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628

R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens] //1.6e-89:468:95//Hs.5117:AA831530

R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623

R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630

R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264

R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258

R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223

R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044

R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224

R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans] //0.30:253:58//Hs.97184:AA385934

R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985

R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621

R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917

R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616

R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332

R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406

R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925

R-NT2RP3004480

R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504

R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens] //3.4e-100:508:95//Hs.47393:AA218858

R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735

R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus] //1.8e-83:465:92//Hs.137064:AA318257

R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971

R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865

R-aaaaaaaaaaaaaa

R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232

R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461

R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674

R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493

R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456

R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213

R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157

R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723

R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680

R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335

R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560

R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219

R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266

R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens] //8.3e-98:462:99//Hs.10114:AI345945

R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030

R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287

R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538

R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:AB007952

R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014

R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294

R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436

R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295

R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569

R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257

R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:AB014600

R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788

R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390

R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185

R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP1)//2.9e-70:354:96//Hs.155481:AJ006470

R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757

R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:AF091092

R-NT2RP4000263

R-nnnnnnnnnnnnn//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//4.7e-104:525:96//Hs.152069:AA548972

R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631

R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99/
/Hs.13410:AF070524

R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760

R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390

R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.
6e-111:520:99//Hs.107479:AB018281

R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-110:527:98//Hs.31323:AF044195

R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130

R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498

R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376

R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk3
0b3.5 [C.elegans]//3.9e-87:499:91//Hs.26156:AA630975

R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN
IN RPS7A-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-95:46
8:96//Hs.93871:AI191318

R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011

R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955

R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953

R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783

R-nnnnnnnnnnnnn//ESTs//4.5e-89:455:96//Hs.62638:AA127740

R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167

R-nnnnnnnnnnnnn

R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05
D3.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:AI424792

R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713

R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U1086

R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874
 R-NT2RP4000519
 R-NT2RP4000524//ESTs, Highly similar to rsec8 [R.norvegicus] //3.4e-93:49
 6:93//Hs.107394:H07126
 R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213
 R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328
 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.nor
 vegicus] //8.2e-92:448:98//Hs.25597:H93026
 R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840
 R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263
 R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531
 R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393
 R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704
 R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651
 R-NT2RP4000724//ESTs//1.5e-83:442:94//Hs.142114:AA205615
 R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399
 R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211
 R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312
 R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.
 1e-106:550:94//Hs.25132:AB007939
 R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834
 R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028
 R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104
 R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356
 R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185
 R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617
 R-nnnnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594
 R-nnnnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI277106
 R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens] //5.9e-17:13

4:85//Hs.14146:W92235

R-nnnnnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA984683

R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,
partial cds//8.2e-108:548:95//Hs.24812:AF069532

R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905

R-NT2RP4000955//ESTs//3.5e-10:119:78//Hs.42946:N21111

R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986

R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179

R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017

R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98/
/Hs.12457:AF052123

R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018

R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620

R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
lete cds//1.1e-28:439:68//Hs.129735:AF010144

R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769

R-NT2RP4001006//ESTs, Moderately similar to ORF2: function unknown [H.sa
piens]//6.6e-124:574:99//Hs.47393:AA218858

R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI418635

R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI336292

R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLA
SMIC [Saccharomyces cerevisiae]//3.6e-114:569:96//Hs.6762:AA088424

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94/
/Hs.100955:AB007859

R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]//2.1e-103:
485:99//Hs.10114:AI345945

R-NT2RP4001078

R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase,
partial//1.7e-119:569:98//Hs.106778:AJ010953

R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164.
R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:AI344055
R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617
R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737
R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357
R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476
R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890
R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [*Saccharomyces cerevisiae*]//5.4e-113:573:96//Hs.5249:U55977
R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453
R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171
R-NT2RP4001150//ESTs//1.9e-90:422:100//Hs.125490:AI138884
R-NT2RP4001159
R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278
R-nnnnnnnnnnnnn//ESTs//1.1e-25:140:97//Hs.83756:AI002822
R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514
R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495
R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [*Homo sapiens*]//4.4e-123:624:95//Hs.22744:AI379892
R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750
R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103
R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120
R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255
R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430
R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933
R-nnnnnnnnnnnnn//ESTs//2.9e-34:213:91//Hs.43100:AA186588

R-NT2RP4001313

R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892

R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612

R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732

R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837

R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616

R-NT2RP4001372

R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN
TRK2-MRS4 INTERGENIC REGION [*Saccharomyces cerevisiae*]//1.7e-108:546:96/
/Hs.32271:AA203680

R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299

R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501

R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN
PAP1-MRPL13 INTERGENIC REGION [*Saccharomyces cerevisiae*]//3.8e-79:438:9
3//Hs.21938:W81045

R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132

R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649

R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [*H.sapiens*]//1.6e
-102:498:97//Hs.62386:AA512948

R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339433

R-NT2RP4001447

R-NT2RP4001474

R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655

R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846

R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511

R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385

R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [*C.elegans*]//2.9e-107:5
46:96//Hs.5570:AI377863

R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292

R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C
 HAIN 5 [Paramecium tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928
 R-NNNNNNNNNNNN//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68
 [S.cerevisiae]//1.4e-26:184:88//Hs.136189:AA133224
 R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552
 R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285
 R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437
 R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251
 R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906
 R-NT2RP4001575
 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOC
 HONDRIAL [S.cerevisiae]//8.7e-112:557:97//Hs.7558:AA526812
 R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776
 R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657
 R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737
 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e
 -116:559:97//Hs.5332:AF007151
 R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:19
 2:97//Hs.5662:AA868361
 R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R
 06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20
 472:W28734
 R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805
 R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete seque
 nce//5.7e-118:583:96//Hs.15562:U96629
 R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941
 R-NNNNNNNNNNNN//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSY
 LTRANSFERASE PRECURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:AI141
 922

R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692

R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:
X78926

R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315

R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien
s] //2.0e-62:326:94//Hs.110839:W28098

R-NT2RP4001803

R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133

R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434

R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826

R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663

R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210

R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:8
8//Hs.154326:D42087

R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602

R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528

R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606

R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099

R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848

R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436

R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793

R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73
919:X81637

R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanog
aster] //8.3e-87:457:94//Hs.41793:AA775879

R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252

R-NT2RP4002018

R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseud
omonas fluorescens] //4.7e-09:90:86//Hs.41127:AA555184

R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738
R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106
R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679
R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198
R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens] //1.6e-61:464:82//Hs.144228:N99507
R-nnnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN CO 8B11.3 IN CHROMOSOME II [C.elegans] //2.3e-56:271:100//Hs.6185:AA428565
R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407
R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592
R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555
R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus] //1.9e-65:373:92//Hs.31532:H18272
R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090
R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934
R-OVARC1000004
R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929
R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635
R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273
R-OVARC1000017
R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286
R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073
R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041
R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367
R-OVARC1000071//ESTs//2.5e-60:321:96//Hs.25010:R67871
R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL0312

R-nnnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703
R-OVARC1000091//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens] /
/3.9e-112:596:94//Hs.20597:W58370
R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942
R-OVARC1000106
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48
-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250
R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:48
9:74//Hs.101238:Y11312
R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482
R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214
R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090
R-OVARC1000151
R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023
R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629
R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339
:81//Hs.154103:AF061258
R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sa
piens] //1.1e-32:196:92//Hs.64322:AA142864
R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874
R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958
R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130
R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN
CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93
//Hs.108117:AI097079
R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476
R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MO
V10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777
R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449

R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743
 R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptid
 e 1C [R.norvegicus] //1.3e-98:488:96//Hs.125749:AI377682
 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863
 R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928
 R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211
 :79//Hs.108287:L27670
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034
 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426
 R-OVARC1000437
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA,
 complete cds//4.3e-45:320:84//Hs.73614:U83460
 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.
 6e-79:418:94//Hs.12334:AB014583
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576
 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211
 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus] //1.1e-102:
 514:96//Hs.11833:AI299947
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983
 R-OVARC1000496
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484
 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs

.155464:AF088219

R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens] //8.5e-48:264:92//Hs.49860:AA702248

R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021

R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106

R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285

R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587

R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627

R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219

R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053

R-OVARC1000605

R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.159897:AB007970

R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:AB011162

R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480

R-nnnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522

R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875

R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517

R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901

R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461

R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans] //1.7e-17:137:86//Hs.7049:AI141736

R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF
 -2 alpha kinase [D.melanogaster] //4.6e-28:430:69//Hs.42457:AA523306
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:9
 5//Hs.3069:L11066
 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.
 2e-106:536:95//Hs.61628:Y17711
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73
 919:X81637
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//H
 s.18910:AF045584
 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096
 R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN
 ROCC-PTA INTERGENIC REGION [Bacillus subtilis] //7.9e-98:525:93//Hs.10366
 :W21953
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401
 R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350
 R-OVARC1000912
 R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814
 R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127
 R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696
 R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215

R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794
R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971
R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs
.155464:AF088219
R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80/
/Hs.43681:AL022394
R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909
R-OVARC1000984//ESTs, Weakly similar to No definition line found [C.eleg
ans] //3.5e-68:346:96//Hs.25544:AA532784
R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811
R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73/
/Hs.127649:AB007874
R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448
R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
1.7e-28:181:77//Hs.139107:K00629
R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270
R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117
R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630
R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apa
f-1) mRNA, complete cds//2.1e-09:137:74//Hs.77579:AF013263
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:
501:96//Hs.9899:AF099149
R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046
R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384
R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12
962
R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231
R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial

cds//7.3e-97:463:98//Hs.3426:AF082657
 R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844
 R-OVARC1001074
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//
 Hs.103126:U57029
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone I
 MAGE 53337, LLNLC110F1857Q7 (RZPD Berlin) and LLNLC110G0913Q7 (RZPD Berl
 in))//1.4e-96:325:98//Hs.21753:AJ005897
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.
 3e-75:386:95//Hs.26584:AF051782
 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete
 cds//3.9e-37:283:84//Hs.46468:U45984
 R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548
 R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312
 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN
 G ENTRY !!!! [H.sapiens]//2.2e-66:346:95//Hs.53263:AA173226
 R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223
 R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727
 R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200
 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs
 .155464:AF088219
 R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA,
 complete cds//6.6e-64:247:80//Hs.97203:U83171
 R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343
 R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826
 R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025
 R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668
 R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166
R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929
R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708
R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532
R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113
R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8
e-70:334:100//Hs.23763:AB011090
R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73
919:X81637
R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1
.0:147:63//Hs.76494:U41344
R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs
.155464:AF088219
R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNIN
G ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356
R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67
247
R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216
R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90
657
R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844
R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777
R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415
R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.
1e-53:344:72//Hs.153468:AB011147
R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958
R-OVARC1001391
R-nnnnnnnnnnnnn//ESTs//0.0039:48:95//Hs.117964:N20913

R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//
Hs.21586:AB006651

R-OVARC1001419

R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136

R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427

R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345

R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592

R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700

R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694

R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089

R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete
cds//3.0e-117:585:96//Hs.6534:AF016507

R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.
.155464:AF088219

R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539

R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//H
s.6396:AB016492

R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388

R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA/
/4.4e-20:150:89//Hs.155160:AF031166

R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:7
2//Hs.154326:D42087

R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019

R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965

R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78/
/Hs.5158:AB007869

R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659

R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854

R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080

R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784

R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]
//1.2e-27:236:81//Hs.15485:AA046954

R-OVARC1001731//Tropomyosin 4 (fibroblast)//7.9e-74:422:90//Hs.102824:XO
5276

R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.
7e-62:300:83//Hs.144563:AF057280

R-nnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [
S.cerevisiae]//6.8e-100:540:92//Hs.117741:AA903456

R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eI
F3, p35 subunit mRNA, complete cds//1.1e-109:567:94//Hs.155377:U97670

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.
0e-109:529:97//Hs.15869:AB014575

R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127

R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604

R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978

R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81/
/Hs.153563:AF011333

R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688

R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831

R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1
e-15:519:63//Hs.25639:AB011110

R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705

R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621

R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160

R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809

R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-
105:571:91//Hs.25300:AF070611

R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476

R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.
2e-49:302:90//Hs.153468:AB011147

R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310

R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749

R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435

R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855

R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842

R-OVARC1001928

R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [*S.cerevisiae*]//2.5e-39:253:88//Hs.117741:AA903456

R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637

R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [*Homo sapiens*]//8.3e-96:498:94//Hs.22744:AI379892

R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875

R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729

R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887

R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531

R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934

R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556

R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315

R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860

R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130

R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [*Caenorhabditis elegans*]//1.7e-102:485:98//Hs.137516:AA805691

R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825

R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923
 R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631
 R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160
 R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478
 R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337
 R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920
 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557
 R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223
 R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870
 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440
 R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503
 R-PLACE1000050//ESTs//9.7e-90:453:96//Hs.27410:N25612
 R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499
 R-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-61:331:94//Hs.30026:AI356771
 R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659
 R-PLACE1000081
 R-PLACE1000094
 R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505
 R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//5.5e-103:538:94//Hs.9670:AA632135
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.151017:AF058291
 R-PLACE1000185//ESTs, Weakly similar to No definition line found [C.elegans]//2.0e-19:114:95//Hs.7036:W22072
 R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:AI262946

R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916
R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U
17077
R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545
R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912
R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940
R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424
R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126
R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:AI334994
R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708
R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959
R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089
R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799
R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125
R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131
R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long fo
rm (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF023456
R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb pr
ecursor [H.sapiens]//2.0e-58:410:81//Hs.97579:AA398118
R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793
R-PLACE1000481//ESTs, Weakly similar to Ndr protein kinase [H.sapiens]//
3.2e-109:549:95//Hs.19074:U69566
R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog
r-vps33b [R.norvegicus]//3.5e-83:435:94//Hs.26510:AA700425
R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729
R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2
e-32:208:88//Hs.153026:AB014540
R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN
IXR1-TFA1 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-26:220:81//

Hs.163791:W25348

R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:A1380485

R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353

R-nnnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542

R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030

R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087

R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301

R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308

R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896

R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353

R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485

R-PLACE1000716

R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701

R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396

R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [C.elegans]//3.9e-40:224:94//Hs.87889:AA262008

R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548

R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482

R-nnnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.2014
4:AF088219

R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189

R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory pr
otein [H.sapiens]//7.7e-31:220:86//Hs.117576:R33135

R-nnnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588

R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039

R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN
YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118:AI141558

R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846

R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091

R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697

R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941

R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689

R-PLACE1000979

R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725

R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:34
3:93//Hs.5662:AA868361

R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146

R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878

R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736

R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762

R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120

R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124

R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580

R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259
:59//Hs.31575:AF100141

R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268

R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610

R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594
R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834
R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H. sapiens] //0.91:77:71//Hs.115211:AA287527
R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297
R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus] //1.9e-99:512:94//Hs.24884:AA176812
R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464
R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131
R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371
R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780
R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460
R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus] //2.7e-22:181:84//Hs.48320:AA149548
R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens] //4.2e-34:195:92//Hs.86276:W27601
R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056
R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//Hs.50984:U01160
R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077
R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615
R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419
R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280

R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555
 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//
 2.6e-45:242:95//Hs.110404:AF091087
 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800
 R-PLACE1001440
 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115
 R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547
 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625
 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617
 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361
 R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds//2.1e-57:339:90//H
 s.4742:AB006969
 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265
 R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431
 R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249
 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601
 R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904
 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1
 e-42:217:97//Hs.75258:AF054174
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sa
 piens]//1.5e-78:458:91//Hs.114547:AA167095
 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526
 R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640
 R-PLACE1001672//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804

R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250

R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124

R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903

R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667

R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993

R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171

R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113

R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266

R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479

R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937

R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243

R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662

R-PLACE1001761

R-PLACE1001771//ESTs//0.92:165:62//Hs.47387:N51980

R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236

R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//1.3e-93:463:95//Hs.40820:AF058953

R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219

R-PLACE1001845

R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868

R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009

R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098

R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936

R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.
85:130:66//Hs.151406:AB014523

R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941

R-PLACE1002046

R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595

R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094

R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619

R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552

R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632

R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311

R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293

R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937

R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614

R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMO
LOG [H.sapiens] //3.6e-39:400:76//Hs.162172:AA534189

R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965

R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745

R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793

R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788

R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892

R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257

R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8
e-67:501:81//Hs.23094:M19503

R-PLACE1002319//ESTs//1.4e-28:178:92//Hs.7353:AA209308

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6
e-95:501:93//Hs.18277:AB018271

R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291

R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381

R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959
R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110
R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60
//Hs.83715:X69804
R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333
R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320
R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:16
6:85//Hs.19368:U69263
R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STA
M2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273
R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429
R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83/
/Hs.5158:AB007869
R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING E
NTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1
e-88:582:85//Hs.88756:AB018256
R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19
:116:93//Hs.99348:AC004774
R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosoph
ila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437
R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131
R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738
R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778
R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus inf
luenzae]//1.2e-44:228:97//Hs.7527:AA843208
R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147

R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749
R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)
//1.0:189:58//Hs.75703:J04130
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternativ
ely spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180
R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830
R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled recep
tor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586
R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865
R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099
R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014
R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392
R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sa
piens]//2.1e-42:233:94//Hs.61518:AA167094
R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756
R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762
R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332
R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
R-PLACE1002962
R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
R-PLACE1002993//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING EN
TRY !!!! [H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268
R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268

R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499
R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156:60//
Hs.82042:D87075
R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840
R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
R-PLACE1003100//ESTs, Highly similar to MODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.6318:AI131178
R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//
Hs.49346:U51920
R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467
R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924
R-PLACE1003176
R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453
R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017
R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802
R-PLACE1003238//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:43
6:94//Hs.58561:W79123
R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460
R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131
R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326
R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986
R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993
R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !

!!! [H.sapiens] //3.3e-94:463:97//Hs.155050:AA908765
R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438
R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715
R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636
R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234
R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans] //3.5e-18:109:95//Hs.27670:AI051591
R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941
R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909
R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755
R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697
R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671
R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270
R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952
R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505
R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980
R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461
R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens] //7.4e-69:338:98//Hs.110439:N93209
R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321
R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591
R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956
R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapie

ns] //1.5e-14:264:65//Hs.158253:R86178
R-PLACE1003584
R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542
R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens] //5
.8e-75:459:89//Hs.23884:AI377106
R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875
R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88/
/Hs.56851:D83200
R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299
R-nnnnnnnnnnnnnn//ESTs//1.0:78:71//Hs.101248:T26446
R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943
R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285
R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247
R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607
R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521
R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866
R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639
R-PLACE1003723//ESTs//1.7e-89:448:96//Hs.157222:AA766987
R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087
R-PLACE1003760//Human globin gene//1.9e-98:538:91//Hs.100090:M69023
R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512
R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302
:U88965
R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798
R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans] //3.8e-38:199
:97//Hs.115197:AA215757
R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909
R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.
2e-36:236:88//Hs.153468:AB011147

R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
G ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092
R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059
R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058
R-PLACE1003864
R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871
R-nnnnnnnnnnnnn
R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595
R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915
R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259
R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.
5e-54:282:96//Hs.58553:AA100804
R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760
R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236
R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110
R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567
R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330
R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231
R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052
R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770
R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244
R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714
R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:49
1:76//Hs.113283:AF018080
R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601
R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11
(COX11) mRNA, complete cds//4.7e-78:434:91//Hs.153504:AF044321
R-PLACE1004197
R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precur

sor, mRNA; complete cds//1.5e-105:501:98//Hs.24640:AF069493
 R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952
 R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630
 R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209
 R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:
 J00124
 R-PLACE1004270//ESTs//0.011:264:59//Hs.110044:AA181800
 R-PLACE1004274//Human retinoic acid receptor-beta associated open readin
 g frame, complete sequence//0.28:121:66//Hs.1938:S82362
 R-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, c
 omplete cds//1.4e-107:581:91//Hs.127007:AF084830
 R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114
 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//2.9e-28:279:77//Hs.38687:AA744496
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cere
 visiae]//8.2e-61:313:95//Hs.71435:AI253099
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:
 590:94//Hs.11171:Y11588
 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducibl
 e), polypeptide 2//6.7e-69:572:77//Hs.1361:M55053
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1
 mRNA, complete cds//7.7e-72:379:93//Hs.16232:AF100153
 R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309
 R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-b
 inding site motif [C.elegans]//1.3e-98:572:90//Hs.14202:N46000
 R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467
 R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665
 R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101

R-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283

R-PLACE1004451

R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980

R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721

R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578

R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194

R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:278:61//Hs.89663:L13286

R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117

R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493

R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164

R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553

R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.115325:D84488

R-PLACE1004550

R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742

R-PLACE1004629//ESTs, Weakly similar to OS-9 precursor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181

R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903

R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734

R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257

R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.8e-90:510:91//Hs.80019:AF035606

R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482
R-PLACE1004686
R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374
R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans] //3.4e-80:413:94//Hs.23528:AI279571
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997
R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N63911
R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619
R-nnnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374
R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367
R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250
R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356
R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.73821:M35663
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185
R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901
R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae] //6.5e-71:381:93//Hs.8383:AA013272
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308

R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456

R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI281881

R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597

R-PLACE1004913//ESTs//4.5e-75:375:96//Hs.91115:AI221563

R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI424948

R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.17839:AF099936

R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980

R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702166

R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013

R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106

R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789

R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI291776

R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335

R-PLACE1005026

R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145:66//Hs.11215:N56719

R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:AB011147

R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543:95//Hs.18625:AI074605

R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103

R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985

R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080

R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364
 R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99
 :531:92//Hs.75437:L40401
 R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336
 R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.
 2e-40:232:82//Hs.155344:U91985
 R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225
 R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423
 R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349
 R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013
 R-PLACE1005176//ESTs//5.4e-75:366:97//Hs.48119:AA454227
 R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589
 R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830
 R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211
 R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532
 R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767
 R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524
 R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633
 R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516
 R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322
 R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937
 R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797
 R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614
 R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:
 94//Hs.136309:AB007960
 R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343
 R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442
 :97//Hs.70202:AA732975
 R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901

R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80/
/Hs.43681:AL022394

R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978

R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304

R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423

R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3
e-88:561:86//Hs.23094:M19503

R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e
-80:549:83//Hs.78935:U29607

R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046

R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875

R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:
319:59//Hs.62705:AB000220

R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cd
s//5.4e-57:277:98//Hs.28307:AF071185

R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325

R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP
)//8.9e-20:321:69//Hs.155481:AJ006470

R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325

R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K1
2H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458:98//Hs.381
14:N62927

R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555

R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PRO
TEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W8
1261

R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835

R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612

R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023

R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927
 R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857
 R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964
 R-PLACE1005630
 R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452
 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete
 cds//1.0e-111:585:93//Hs.8765:AF083255
 R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169
 R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2
 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587
 R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355
 R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332
 R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259
 R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protei
 n [M.musculus]//1.3e-42:236:94//Hs.23889:AI341137
 R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070
 R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:8
 7//Hs.154326:D42087
 R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK
 757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:88:98//Hs.1098
 57:AA088385
 R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941
 R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327
 R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI287693
 R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058
 R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58/
 /Hs.75770:L41870
 R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI050965
 R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471

R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305
R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI339981
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI341793
R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8
e-27:382:70//Hs.23094:M19503
R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:37
7:93//Hs.5662:AA868361
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI183729
R-PLACE1005953
R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN
CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88
//Hs.108117:AI097079
R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:AI016239
R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897
R-PLACE1005990
R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:
74//Hs.153014:AB002353
R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN
APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:5
93:93//Hs.111449:AI192946
R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERAS
E [D.melanogaster]//5.7e-100:596:88//Hs.24284:AA595596
R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:AI056276
R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:49

1:98//Hs.61164:AI096332
R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765
R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
G ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007:H74314
R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904
R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002
R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN
SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:
91//Hs.5249:U55977
R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glyco
gen debranching enzyme, glycogen storage disease type III)//0.038:463:59
//Hs.904:U84010
R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:AI357886
R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925
R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128
R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:9
4//Hs.152894:AC005239
R-nnnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicu
s]//2.7e-79:393:96//Hs.19121:AI125280
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:
95//Hs.30464:AF091433
R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//6.8e-94:532:91//Hs.105216:AI361807
R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507
R-PLACE1006205//EST//1.7e-89:448:96//Hs.116665:AA669114
R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.9
0:304:58//Hs.94986:U77664
R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI079555
R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472

R-nnnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142
R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.m usculus]//1.3e-104:532:95//Hs.41151:AI301961
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548
R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321:62//Hs.53057:W67839
R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132
R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265
R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503
R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900
R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168
R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044
R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI079284
R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053
R-PLACE1006382
R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748
R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI281881
R-PLACE1006414//Homo sapiens LIM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258
R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI278629
R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139
R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961
R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297
R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418
R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722

R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374
 R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:
 63//Hs.48824:D87717
 R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723
 R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368
 R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532
 R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214
 R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eI
 F3, p35 subunit mRNA, complete cds//9.3e-118:590:95//Hs.155377:U97670
 R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322
 R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615
 R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:
 78//Hs.101359:AB002384
 R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522
 R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627
 R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736
 R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98/
 /Hs.12472:AF038172
 R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861
 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//
 Hs.7252:AF070622
 R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658
 R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234
 R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515
 R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335
 R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989
 R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847

R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159
 R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO
 MOLOG [Homo sapiens] //1.0e-87:481:92//Hs.141263:H64113
 R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933
 R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA828359
 R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008
 R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536
 R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131
 R-nnnnnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348
 R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089
 R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13
 168
 R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514
 R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078
 R-nnnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:
 63//Hs.36927:D86956
 R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X5252
 0
 R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens] //
 9.0e-29:324:68//Hs.154257:AI275982
 R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636
 R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257
 R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366
 R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971
 R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6
 e-83:584:82//Hs.23094:M19503
 R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575
 R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027
 R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202

R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646
 R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417
 R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948
 R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794
 R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765
 R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998
 R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619
 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495
 R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H.sapiens] /
 /3.7e-73:357:98//Hs.18272:N78499
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909
 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:AI275071
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087
 R-PLACE1007301
 R-PLACE1007317
 R-PLACE1007342
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870
 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //2.2e-98:488:96//Hs.24359:AA699594
 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877

R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771

R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.72165:AI243857

R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171

R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514

R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230

R-PLACE1007478

R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975

R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker type s), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533

R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072

R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657

R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377

R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087

R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612

R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404

R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840

R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257

R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179

R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923

R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176

R-PLACE1007632
R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106
R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946
R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNI
NG ENTRY !!!! [H.sapiens]//9.0e-37:190:97//Hs.23437:AA707331
R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944
R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C
HAIN 5 [Ascaris suum]//3.4e-61:384:89//Hs.92918:AA133274
R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces ce
revisiae]//1.8e-84:501:88//Hs.91251:U66685
R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds
//0.43:307:59//Hs.54481:D86407
R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/
/5.7e-75:374:96//Hs.4812:AF061243
R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.eleg
ans]//3.1e-39:253:88//Hs.108797:AA476815
R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619
R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.
7e-94:556:89//Hs.153121:AB014585
R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322
R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778
R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903
R-PLACE1007791//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTE
IN A [Bacillus subtilis]//8.6e-27:143:98//Hs.144194:AA706337
R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9
e-45:428:76//Hs.23094:M19503
R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044
R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050
R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839

R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503

R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017

R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:AB018309

R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178

R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832

R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060

R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.92381:AB007956

R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510

R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966

R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.5671:AF084530

R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:465:93//Hs.78106:AF079529

R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900

R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]//3.8e-97:493:95//Hs.6141:U69564

R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835

R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612

R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]//2.0e-115:575:95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935

R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269

R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469

R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334

R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6
 e-104:551:93//Hs.10801:AB011102
 R-PLACE1008209//ESTs//1.2e-72:366:96//Hs.92308:AI052701
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
 R-nnnnnnnnnnnnn
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.5
 3:206:62//Hs.79070:K02276
 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.
 sapiens] //8.6e-79:297:91//Hs.146477:AI128445
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1
 e-99:556:90//Hs.5734:AB014579
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052
 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
 G ENTRY !!!! [H.sapiens] //2.0e-41:448:72//Hs.139007:H74314
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169
 :AA156242
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT

RY !!!! [H.sapiens] //1.2e-81:536:87//Hs.7570:W31010
R-nnnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:9
5//Hs.7763:D86326
R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778
R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757
R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562
R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928
R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636
R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
R-PLACE1008532
R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223
R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens] /
/8.6e-67:483:82//Hs.140416:AA778649
R-nnnnnnnnnnnnn
R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972
R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512
R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612
R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:
79//Hs.153014:AB002353
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, compl
ete cds//7.9e-90:434:97//Hs.147967:AF044333

R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.
51048:X68830

R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducibl
e), polypeptide 2//1.7e-51:316:76//Hs.1361:M55053

R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600

R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !
!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303

R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408

R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313

R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930

R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217

R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 m
RNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905

R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cml
0e3 [C.elegans]//4.2e-92:490:93//Hs.110454:H11810

R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428

R-nnnnnnnnnnnnnnn

R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502

R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878

R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893

R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6
e-56:344:89//Hs.62318:AB018308

R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018

R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653

R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSP
ORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680

R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573

R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419

R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.3

4780:AJ003112

R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520

R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195

R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139

R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008

R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R1
OE12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9
663:AA527142

R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448

R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:16
1:63//Hs.77608:AL021546

R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.
037:63:84//Hs.39943:AA203136

R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549

R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983

R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapien
s]//6.5e-97:501:94//Hs.11123:AA703945

R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747

R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.
norvegicus]//2.5e-36:163:82//Hs.93332:AA811920

R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005

R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322

R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948

R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707

R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717

R-PLACE1009186//ESTs, Weakly similar to No definition line found [C.eleg
ans]//1.5e-109:572:94//Hs.54943:Z78396

R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701

R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X

98248

R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680

R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018

R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423

R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279

R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3
e-82:578:82//Hs.23094:M19503

R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397

R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782

R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760

R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA161260

R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883

R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186

R-nnnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798

R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255

R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632

R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269

R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.
76987:AF012872

R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427

R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.
3e-42:266:89//Hs.155049:AC004531

R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925

R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596

R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698

R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131

R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apa
f-1) mRNA, complete cds//1.4e-10:289:63//Hs.77579:AF013263

R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326

R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHA
IN PRECURSORS [H.sapiens] //0.0012:56:91//Hs.12151:AA001818

R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.
0e-42:547:70//Hs.69157:AB014535

R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735

R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482

R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680

R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243338

R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858

R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701

R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.
3e-109:589:92//Hs.21862:AB011159

R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens] /
/9.9e-62:483:79//Hs.140416:AA778649

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:31
0:97//Hs.109590:AF062534

R-PLACE1009708//ESTs//3.0e-94:471:96//Hs.40091:N48582

R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae] //4.2
e-98:529:92//Hs.3945:AA004210

R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.
musculus] //6.8e-85:489:89//Hs.26194:AA033989

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:59
8:95//Hs.154320:AF046024

R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989

R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25
-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3,
EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein
Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part o

f a novel gene similar to hypothetical proteins *S. pombe* C22F3.14C and *C. elegans* C16A3.8. Contains ESTs and GSSs//1.1e-113:549:97//Hs.16411:AL030996

R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868

R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748

R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328

R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031

R-nnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [*C.elegans*]//1.6e-114:594:94//Hs.67466:AI219740

R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563

R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276

R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI304317

R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543

R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074

R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:AI160540

R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347

R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219

R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [*C.elegans*]//1.7e-17:137:86//Hs.7049:AI141736

R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204

R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [*M.musculus*]//7.6e-104:546:94//Hs.8215:AA521150

R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905

R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.11183:AF065482

R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375

R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424

R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615
R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.no
rvegicus]//2.8e-104:565:92//Hs.11469:U69567
R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015
R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103
R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-
107:575:93//Hs.48301:AA122270
R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130
R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359
R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897
R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313
R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466
R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037
R-PLACE1010231
R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478
R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545
R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535
R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788
R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081
R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568
R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs
.155464:AF088219
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING
ENTRY !!!! [H.sapiens]//9.9e-32:190:77//Hs.152369:AA504818
R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327
R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594
R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, p
artial//4.9e-35:166:86//Hs.53531:AJ224162
R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152

R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:AF039081
R-PLACE1010492
R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031
R-nnnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455
R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306
R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033
R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116
R-PLACE1010599
R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418
R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895
R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475
R-PLACE1010628//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:391:95//Hs.163495:W57637
R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805
R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102
R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:91//Hs.22383:R51067
R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794:AA701659
R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973
R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943
R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mR

NA, partial cds//1.2e-56:300:95//Hs.50758:AF092564
R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189
R-PLACE1010743
R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250
R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024
R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]//7.6e-111:575:94//Hs.10260:AI126627
R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558
R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:AI091203
R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896
R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472
R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048
R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917
R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182
R-PLACE1010891
R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983
R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023
R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630
R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093
R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126

R-nnnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//
8.9e-82:441:93//Hs.66392:AF064244
R-PLACE1010944
R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519
R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs
.155464:AF088219
R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosoph
ila melanogaster]//1.0e-103:565:92//Hs.23259:AA532437
R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580
R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846
R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867
R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4
e-102:563:91//Hs.41143:AB011153
R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135
R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs
.155464:AF088219
R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537
R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//1.6e-54:398:84//Hs.108740:W20094
R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478
R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA099587
R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease vi
rus]//3.0e-105:552:93//Hs.31257:AA875998
R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795
R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:5
34:91//Hs.28719:AB015333
R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673
R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !

!!! [H.sapiens] //3.4e-85:442:95//Hs.136910:AA810782
R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438
R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671
R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299
R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693
R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602
R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772
R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913
R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849
R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807
R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572
:U79291
R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTE
IN A [Bacillus subtilis] //3.4e-92:452:97//Hs.144194:AA706337
R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376
R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194
R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8
e-114:600:94//Hs.10801:AB011102
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7
e-32:310:76//Hs.138488:AB014607
R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.
6e-104:515:96//Hs.111138:AB018255
R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.2
8197:AF035294
R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576

R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421
 R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985
 R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs
 .8597:L11672
 R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61
 //Hs.78344:AF001548
 R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067
 R-PLACE1011641//ESTs//2.5e-71:338:100//Hs.153085:AA993965
 R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900
 R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//
 Hs.78019:AF070535
 R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036
 R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filam
 ent-associated protein)//0.50:178:62//Hs.31638:X64838
 R-PLACE1011675
 R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025
 R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5
 e-57:410:83//Hs.23094:M19503
 R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392
 R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426
 R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative product
 s} //7.3e-40:361:77//Hs.53217:Z48051
 R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
 3.0e-60:319:76//Hs.103948:K00627
 R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080
 R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF06
 8179
 R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563
 R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:8

0//Hs.22271:D26067
 R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648
 R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913
 R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI275497
 R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268
 R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//
 2.3e-99:546:92//Hs.3838:AF059617
 R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI031969
 R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM
 OLOG [H.sapiens] //2.6e-06:284:63//Hs.124102:AA701285
 R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890
 R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0
 e-106:540:95//Hs.88756:AB018256
 R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069
 R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//
 4.8e-105:524:95//Hs.21811:AF091080
 R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211
 R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504
 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mR
 NA//1.6e-43:355:79//Hs.154069:U06452
 R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013
 R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-4
 5:514:72//Hs.96247:X95073
 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated mo
 lecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622
 R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652

R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.
2e-41:429:72//Hs.153468:AB011147
R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:8
6//Hs.40100:AB002390
R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6
.2e-111:550:95//Hs.9443:AF027219
R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF06
8179
R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236
R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941
R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA,
partial cds//0.00043:127:71//Hs.42400:AF022789
R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662
R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988
R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558
R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.
7e-44:302:85//Hs.118401:AB011134
R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357
R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs
.155464:AF088219
R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778
R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292
R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:9
0//Hs.22271:D26067
R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:AI382378
R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191
R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717
R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.807
06:M81600

R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363

R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:AI004779

R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOSOLIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664

R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:AI344055

R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380

R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058

R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789

R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618

R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848

R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081

R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731

R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277

R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781

R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189

R-PLACE2000399

R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOSOLIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA088424

R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941

R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739

R-PLACE2000425//Homo sapiens DEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333

R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEE
SI42F [C.elegans] //3.0e-113:543:97//Hs.16933:AA976002

R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523

R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986

R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887

R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:7
4//Hs.40100:AB002390

R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714

R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638

R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228

R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642

R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838

R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.
3e-64:350:86//Hs.153468:AB011147

R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763

R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979

R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.
51048:X68830

R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727

R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739

R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792

R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369

R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142

R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815

R-PLACE3000155//ESTs//1.2e-19:192:79//Hs.131350:AA805223

R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen n
ecrosis virus] //4.8e-36:262:88//Hs.31532:H18272

R-PLACE3000157

R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs

.155464:AF088219

R-PLACE3000160

R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798

R-PLACE3000194

R-PLACE3000197//ESTs//1.4e-38:197:98//Hs.146341:AI269930

R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus
scrofa] //0.018:261:61//Hs.131370:AA927516

R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476

R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084

R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964

R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717

R-PLACE3000226//ESTs//1.3e-49:269:95//Hs.9059:AI359014

R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878

R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.7
6313:U04811

R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [
Emericella nidulans] //7.5e-110:549:95//Hs.13692:AA632002

R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:9
4//Hs.87908:AB002307

R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA,
complete cds//2.3e-62:287:82//Hs.97203:U83171

R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782

R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phos
phate 5-kinase (PIPK) mRNA, complete cds//4.0e-59:456:80//Hs.108966:U486
96

R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.
51048:X68830

R-PLACE3000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627

R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo s

apiens] //5.8e-34:190:95//Hs.114531:N74103
R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.
7e-32:239:84//Hs.15519:AB018315
R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837
R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688
R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:2
91:76//Hs.1721:X58377
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888
R-PLACE3000363
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens] //1.0e-35:427:73//Hs.138795:R98534
R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.
142570:AF052160
R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:31
5:82//Hs.37181:D64108
R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA,
complete cds//4.4e-47:302:87//Hs.73614:U83460
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs
.155464:AF088219
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs
..32567:AF073519

R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.153487:U43899
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227
R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:AB018352
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292
R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739
R-PLACE4000100
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:AB007931
R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-11:184:71//Hs.154278:N45985
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.118164:AB007969
R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:AB011147
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186
R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080

R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219

R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216

R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442

R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586

R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782

R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131

R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454

R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460

R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414

R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478

R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656

R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425

R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-44:379:78//Hs.152369:AA504818

R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:AA778649

R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502

R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780

R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:AA643063

R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:72//Hs.1361:M55053

R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932

R-PLACE4000494//ESTs//1.4e-109:525:98//Hs.22539:AI334210

R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290

R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527

R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185

R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532

R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524

R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249

R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889

R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651

R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438

R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435

R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353

R-THYRO1000107//Interleukin 10//2.8e-43:292:84//Hs.2180:M57627

R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO MOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359

R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108

R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764

R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:AF087142

R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN G ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217

R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426

R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258

R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946

R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189

R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219

R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs

.155464:AF088219

R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6
e-110:535:97//Hs.43445:AJ005698

R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.
3e-115:559:97//Hs.79672:AB014552

R-THYR01000206//ESTs//3.1e-90:507:90//Hs.32456:W29063

R-THYR01000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349

R-THYR01000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.
8e-69:524:82//Hs.141874:AB014588

R-THYR01000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYR01000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80/
/Hs.80738:X52075

R-THYR01000270//ESTs//1.9e-99:531:94//Hs.17767:N62925

R-THYR01000279//EST//2.7e-54:266:99//Hs.149527:AI280674

R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:
566:91//Hs.25846:AB016068

R-THYR01000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547

R-THYR01000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.8
0731:M63175

R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4
e-113:559:96//Hs.12002:AB018333

R-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds
//1.5e-48:317:87//Hs.7833:U29091

R-THYR01000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064

R-nnnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250

R-THYR01000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mR
NA, complete cds//4.6e-69:294:84//Hs.151614:AF032456

R-THYR01000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081

R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429
R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601
R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638
R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans] //8.5e-40:239:90//Hs.84009:AI309761
R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426
R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:AB018280
R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333
R-THYRO1000501//ESTs//1.5e-46:287:89//Hs.125300:R62360
R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005
R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H.sapiens] //3.9e-57:286:96//Hs.105861:AI206965
R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511
R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193
R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485
R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:AF075587
R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247
R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223
R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens] //1.2e-96:483:96//Hs.21907:N24415
R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742
R-THYRO1000637
R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.sapiens] //4.9e-46:245:95//Hs.97398:AA398634
R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840
R-nnnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384

R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI061063
 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713
 R-THYRO1000712
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713
 R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GAL
 ACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens] //8.1e-82:497:87//Hs.1
 09672:W22624
 R-THYRO1000777
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897
 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144
 R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381
 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594
 R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:8
 7//Hs.22271:D26067
 R-THYRO1000829
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
 R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:AI281881
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA
 dependent//2.8e-44:374:79//Hs.73821:M35663
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
 mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182

R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859
R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440
R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881
R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524
R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777
R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131
R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H. sapiens]//3.0e-57:341:91//Hs.44049:AA521489
R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717
R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223
R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
R-THYRO1001100
R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:AI138834
R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417
R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922
R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853
R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
R-THYRO1001177
R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151

R-THYR01001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932
R-THYR01001262//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
1.3e-48:349:83//Hs.139107:K00629
R-THYR01001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D
13640
R-THYR01001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
R-THYR01001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
R-THYR01001320//ESTs//1.4e-61:403:79//Hs.139555:N48230
R-THYR01001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan sy
ndrome)//8.5e-05:326:60//Hs.82314:M31642
R-nnnnnnnnnnnn//ESTs//0.16:422:59//Hs.23876:AA082935
R-THYR01001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:56
2:94//Hs.15032:AA774250
R-THYR01001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
R-THYR01001365
R-THYR01001374
R-THYR01001401//Human HsLIM15 mRNA for HsLim15, complete cds//2.5e-48:46
7:75//Hs.37181:D64108
R-THYR01001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
R-THYR01001405//ESTs//4.8e-25:197:84//Hs.6907:W72733
R-THYR01001406//EST//0.0023:117:66//Hs.162931:AA633197
R-THYR01001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
R-THYR01001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0508//9.1e-49:305:86//Hs.159187:AB007977
R-THYR01001434//ESTs//0.40:161:61//Hs.161993:AA503172
R-THYR01001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
G ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082
R-THYR01001480//Small inducible cytokine A5 (RANTES)//1.3e-40:331:79//Hs
.155464:AF088219

R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.
1e-17:134:76//Hs.15731:AB011135

R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110

R-THYRO1001537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094

R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9
.0e-49:427:76//Hs.2217:U21936

R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594

R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413

R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958

R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741

R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247

R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:28
8:67//Hs.85112:X57025

R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03
886

R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:dihydroxyacetonephosph
ate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs.1248
2:AJ002190

R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83/
/Hs.127649:AB007874

R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282

R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446

R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59
kDa isoform//1.6e-111:562:95//Hs.118633:AJ225089

R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//1.0e-17:246:73//Hs.67619:AB007957

R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726

R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691

R-THYRO1001721
R-nnnnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:14
7:77//Hs.158196:R53184
R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.
116549:AL009172
R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323
R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474
R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224
R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788
R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//5.7e-38:242:83//Hs.92381:AB007956
R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123
R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
G ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314
R-VESEN1000122
R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289
R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI359321
R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178
R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8
e-51:330:89//Hs.153026:AB014540
R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629
R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792
R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.eleg
ans]//2.4e-110:553:95//Hs.23159:AA113849
R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62/
/Hs.79414:D79991
R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103
R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI421812
R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:AI246624

R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:AI092936
 R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:8
 4//Hs.84123:AB002363
 R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826
 R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635
 R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:23
 9:88//Hs.23476:AA401210
 R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808
 R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-bi
 nding protein Spnr [M.musculus]//4.4e-66:339:97//Hs.8215:AA521150
 R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
 G ENTRY !!!! [H.sapiens]//3.2e-44:279:88//Hs.139007:H74314
 R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018
 R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613
 R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758
 R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292
 R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protei
 n AUP46 precursor [M.musculus]//3.1e-60:362:88//Hs.6381:AI188509
 R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320
 R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881
 R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, com
 plete cds//0.95:172:62//Hs.41723:U37426
 R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848
 R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicu
 s]//8.2e-97:482:97//Hs.19121:AI125280
 R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:56
 4:93//Hs.16361:AI147455
 R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete
 cds//3.4e-99:517:94//Hs.60580:AF060503

R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE I
N AT51-TPD3 INTERGENIC REGION [*Saccharomyces cerevisiae*]//8.1e-27:140:10
0//Hs.129049:H28818

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA
, complete cds//8.7e-114:586:95//Hs.83023:AF093670

R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25
B5.5 IN CHROMOSOME III [*C.elegans*]//9.8e-111:563:95//Hs.19845:AI005330

R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1
701:L26405

R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:1
00//Hs.84753:D87433

R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359

R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512

R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642

R-nnnnnnnnnnnnn//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405

R-Y79AA1000805

R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227

R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, comp
lete cds//0.016:386:59//Hs.55836:U85647

R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079

R-Y79AA1000968

R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181

R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049

R-Y79AA1000985

R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851

R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067

R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407

R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325
 R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.
 8e-53:279:83//Hs.15731:AB011135
 R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047
 R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260
 R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155
 R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015
 R-Y79AA1001167
 R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884
 R-Y79AA1001185
 R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051
 R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933
 R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI025750
 R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674
 R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequ
 ence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)
)//1.1e-110:549:95//Hs.23170:AJ005892
 R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271
 R-Y79AA1001299//Human Inil mRNA, complete cds//9.6e-25:133:100//Hs.15562
 6:U04847
 R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:AI191149
 R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084
 R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143
 R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819
 R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859
 R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891
 R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2
 -17 KD 11 [Arabidopsis thaliana]//4.4e-109:553:95//Hs.106616:AI027524
 R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704

R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus] //6.2e-46:260:94//Hs.24884:AA176812

R-nnnnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA868563

R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872

R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177

R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508

R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI126237

R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI336204

R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens] /7.2e-81:400:97//Hs.13323:AA897542

R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486

R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli] //2.5e-19:112:97//Hs.26252:AA643235

R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus] //9.7e-99:553:92//Hs.108896:R54040

R-nnnnnnnnnnnnn

R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA211783

R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA418490

R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12 . Contains part of a gene for a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phospholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251:63//Hs.21864:AL031652

R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans] //9.4e-87:427:97//Hs.18645:AI023798

R-nnnnnnnnnnnnn//ESTs//1.1e-112:558:97//Hs.109755:AA180809

R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.0 3c protein [H.sapiens] //8.1e-95:530:91//Hs.72444:W23217

R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582
R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.
.99931:L34355
R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:AI278630
R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094
R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652
R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404
R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275
R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.
69:93:73//Hs.15731:AB011135
R-Y79AA1002089//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:39
2:80//Hs.113283:AF018080
R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//H
s.78185:L38933
R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:AI417785
R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275
R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399
R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858
R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725
R-nnnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715
R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA syntheta
se. [C.elegans] //3.5e-108:553:95//Hs.50441:AA747428
R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349
R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING
PROTEIN [H.sapiens] //6.5e-86:518:90//Hs.25682:AA857843
R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274
R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0
e-118:564:98//Hs.100729:AB014592

R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME
[D.melanogaster] //9.0e-102:507:96//Hs.25895:AI341537

R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4
e-93:453:97//Hs.96731:AB014555

R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288

R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1
e-110:403:99//Hs.30898:AB014534

R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985

R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371

R-Y79AA1002361

R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908

R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000

R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753

R-Y79AA1002431//EST//6.6e-23:128:98//Hs.128417:AA975026

R-nnnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 6
8 [Saccharomyces cerevisiae] //4.4e-62:390:88//Hs.143930:AI207821

R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870

R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788

R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

【 0 8 2 9 】

相同性検索結果データ 6.

全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データ。以下に示す検索結果には、比較配列の長さの単位にaaとbpが混在している。

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%/Q61712

C-HEMBA1000030

C-HEMBA1000046

C-HEMBA1000050

C-HEMBA1000076

C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%/P08553

C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5E-16//166aa//36%/P35584

C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%/P35662

C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%/P48555

C-HEMBA1000193

C-HEMBA1000227

C-HEMBA1000288

C-HEMBA1000302

C-HEMBA1000304

C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91%/035594

C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%/AL049654

C-HEMBA1000387

C-HEMBA1000392

C-HEMBA1000460

C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%/Q04652

C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%/P22279

C-HEMBA1000501

C-HEMBA1000508

C-HEMBA1000520

C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%/P02826

C-HEMBA1000534

C-HEMBA1000555

C-HEMBA1000568

C-HEMBA1000588

C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179a
a//61%//043295

C-HEMBA1000636

C-HEMBA1000682

C-HEMBA1000686

C-HEMBA1000719

C-HEMBA1000727

C-HEMBA1000752

C-HEMBA1000817

C-HEMBA1000851

C-HEMBA1000867

C-HEMBA1000869

C-HEMBA1000872

C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-X
P ANTIGEN)//1.6E-30//127aa//40%//P43366

C-HEMBA1000918

C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN
F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%//Q19124

C-HEMBA1000946

C-HEMBA1000968

C-HEMBA1000971

C-HEMBA1000975

C-HEMBA1001009

C-HEMBA1001022

C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHR
OID) (FRAGMENT).//1.4E-12//131aa//38%//Q01485

C-HEMBA1001052

C-HEMBA1001080

C-HEMBA1001085

C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%//P48059

C-HEMBA1001109

C-HEMBA1001122

C-HEMBA1001133

C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%//Q06730

C-HEMBA1001140

C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646

C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//AB020678

C-HEMBA1001235

C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733

C-HEMBA1001281

C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401

C-HEMBA1001303

C-HEMBA1001310

C-HEMBA1001326

C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358

C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081

C-HEMBA1001388

C-HEMBA1001398

C-HEMBA1001405

C-HEMBA1001407

C-HEMBA1001413

C-HEMBA1001415

C-HEMBA1001446

C-HEMBA1001450

C-HEMBA1001455

C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850

C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166

C-HEMBA1001533

C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657

C-HEMBA1001581

C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141

C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//Q63679

C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%//P33450

C-HEMBA1001702

C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386

C-HEMBA1001731

C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%//P53009

C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675

C-HEMBA1001815

C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52
%/Q99676

C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%/Q
07230

C-HEMBA1001864

C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%/P20659

C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (M
E2GLYDH).//9.3E-36//395aa//26%/Q63342

C-HEMBA1001987

C-HEMBA1002018

C-HEMBA1002049

C-HEMBA1002084

C-HEMBA1002125

C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-5
1//180aa//56%/P79293

C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E
-13//190aa//36%/P43694

C-HEMBA1002191

C-HEMBA1002199

C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E
-17//267aa//29%/P18161

C-HEMBA1002237

C-HEMBA1002265

C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//
90%/AF125537

C-HEMBA1002349

C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mR
NA, complete cds.//0//1847bp//99%/AF092563

C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%/P22793

C-HEMBA1002430

C-HEMBA1002439

C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//
109aa//55%//Q00994

C-HEMBA1002460

C-HEMBA1002462

C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P9817
5

C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.
1E-12//285aa//31%//P17437

C-HEMBA1002477

C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa
//36%//P48732

C-HEMBA1002515

C-HEMBA1002542

C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete
cds.//6.8E-305//951bp//99%//AF075587

C-HEMBA1002583

C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.
4E-253//1149bp//99%//AB011169

C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0
//1539bp//99%//AB018351

C-HEMBA1002688

C-HEMBA1002696

C-HEMBA1002750

C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
.//1E-80//882bp//61%//AJ000414

C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0/
/1532bp//99%//AB020636

C-HEMBA1002777

C-HEMBA1002794

C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.
s.//8.2e-314//1437bp//99%//AF071185

C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819

C-HEMBA1002850

C-HEMBA1002863

C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//
1.5E-44//188aa//52%//Q09297

C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0/
/1483bp//100%//AB011148

C-HEMBA1002937

C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//
/2E-34//300aa//34%//P16157

C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0/
/1752bp//99%//AB020710

C-HEMBA1002954

C-HEMBA1002971

C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1
.4.17) (DPDE4).//1.2E-27//63aa//100%//P14646

C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa/
/24%//Q02224

C-HEMBA1003033

C-HEMBA1003035

C-HEMBA1003041

C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR
(EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//075439

C-HEMBA1003067

C-HEMBA1003096

C-HEMBA1003117

C-HEMBA1003129

C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP
-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)
./8.5E-51//221aa//33%/P41940

C-HEMBA1003148//Homo sapiens mRNA full length insert cDNA clone EUROIMAG
E 381801./0//1583bp//99%/AL079278

C-HEMBA1003175

C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METH
YLTRANSFERASE (EC 2.1.1.61)./5.9E-74//134aa//53%/P44551

C-HEMBA1003199

C-HEMBA1003222

C-HEMBA1003235//TROPOMYOSIN./0.0000023//109aa//33%/Q02088

C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-)./7.2E-41//245aa//42%/
/Q06548

C-HEMBA1003257

C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR./6E-11//239aa//32%/P3250
6

C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV,
complete cds./5.4E-229//1043bp//99%/AB024436

C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds./0
//791bp//99%/AB011109

C-HEMBA1003322

C-HEMBA1003327

C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN)./0.00000002//248
aa//23%/Q02224

C-HEMBA1003370

C-HEMBA1003380

C-HEMBA1003395

C-HEMBA1003402

C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0
//1732bp//98%//AB020712

C-HEMBA1003417//Homo sapiens mRNA: cDNA DKFZp586C021 (from clone DKFZp58
6C021).//1.6e-312//1414bp//99%//AL050287

C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%//P37709

C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%
//AB013139

C-HEMBA1003447

C-HEMBA1003461

C-HEMBA1003463

C-HEMBA1003528

C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189
//360aa//96%//P50480

C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%//
P53384

C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-
2 SUBUNIT (G GAMMA-I).//1.2E-31//71aa//100%//P16874

C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)
) (RO(SS-A)).//7.9E-49//279aa//32%//P19474

C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74
%//Q13330

C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%//P26039

C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//
4.4E-10//118aa//35%//P19682

C-HEMBA1003615

C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//50
1bp//97%//AB015344

C-HEMBA1003621

C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%//Q1
3207

C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%//P53973

C-HEMBA1003711

C-HEMBA1003807

C-HEMBA1003864

C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAG
MENT).//3.8E-16//89aa//46%//P16372

C-HEMBA1003959

C-HEMBA1003989

C-HEMBA1004074

C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complet
e cds.//8.5E-221//1188bp//78%//AF091234

C-HEMBA1004146

C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0/
/1893bp//98%//AB023145

C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, compl
ete cds.//0//1892bp//99%//U50748

C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete
cds.//5.7E-217//1217bp//88%//AF095927

C-HEMBA1004246

C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, co
mplete cds.//4.8E-257//738bp//99%//AF092094

C-HEMBA1004289

C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512
bp//96%//AF132955

C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1
.2e-316//1445bp//99%//AF089841

C-HEMBA1004596

C-HEMBA1004693

C-HEMBA1004736

C-HEMBA1004753

C-HEMBA1004756//Human transporter protein (gl7) mRNA, complete cds.//9.1
E-34//515bp//66%//U49082

C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds
./2.6E-246//1249bp//94%//L39060

C-HEMBA1004763

C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//
58%//P08547

C-HEMBA1004771

C-HEMBA1004776

C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P508
51

C-HEMBA1004806

C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E
-154//317aa//94%//Q00004

C-HEMBA1004850

C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp5
86M2022).//0//1443bp//100%//AL080114

C-HEMBA1004923

C-HEMBA1004929

C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27
//65aa//100%//Q16401

C-HEMBA1004933

C-HEMBA1004954

C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR
OTEIN) (NF-H).//0.00000096//286aa//23%//P12036

C-HEMBA1005475

C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%//AF133270

C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%//P16372

C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%//AF076183

C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043

C-HEMBA1006377

C-HEMBA1006467

C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552

C-HEMBA1006530

C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.000000043//111aa//40%//Q01485

C-HEMBA1006795

C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258

C-HEMBA1006936

C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//AF078849

C-HEMBA1007342

C-HEMBA1000008

C-HEMBA1000018

C-HEMBA1000024

C-HEMBA1000025

C-HEMBA1000036

C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%//AF084928

C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%

//P11799

C-HEMBB1000103

C-HEMBB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%/Y15521

C-HEMBB1000136

C-HEMBB1000215

C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI
CASE EEED8.5.//2.7E-12//112aa//47%/Q09530

C-HEMBB1000244

C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN
ZC302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%/Q23256

C-HEMBB1000338

C-HEMBB1000339

C-HEMBB1000391

C-HEMBB1000438

C-HEMBB1000449

C-HEMBB1000589

C-HEMBB1000591

C-HEMBB1000623

C-HEMBB1000630

C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTO
R 1).//4.1E-19//232aa//28%/P78970

C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//2
73aa//31%/P27671

C-HEMBB1000671

C-HEMBB1000673

C-HEMBB1000705

C-HEMBB1000706

C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cd
s.//6.2E-130//692bp//93%/U53475

C-HEM BB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676 bp//96%//AF151847

C-HEM BB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.2E-126//613bp//97%//AF111105

C-HEM BB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-54//232aa//43%//P39956

C-HEM BB1000807

C-HEM BB1000810

C-HEM BB1000848

C-HEM BB1000852

C-HEM BB1000870

C-HEM BB1000887

C-HEM BB1000908

C-HEM BB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//59 5bp//76%//AF120102

C-HEM BB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910

C-HEM BB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E -120//580bp//67%//AF099974

C-HEM BB1000975

C-HEM BB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-18//178aa//30%//P28575

C-HEM BB1000991

C-HEM BB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E -73//230aa//45%//P51523

C-HEM BB1001014

C-HEM BB1001024

C-HEM BB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION -ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087

C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//80%//AF010144

C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803

C-HEMBB1001096

C-HEMBB1001105

C-HEMBB1001117

C-HEMBB1001126

C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435

C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267

C-HEMBB1001153

C-HEMBB1001169

C-HEMBB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357

C-HEMBB1001182

C-HEMBB1001199

C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187

C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF 4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897

C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966

C-HEMBB1001289

C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081

C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%//U92703

C-HEMBB1001331

C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98

175

C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA,
nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//29

2bp//99%//AF097441

C-HEMBB1001369

C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds./
/0//1586bp//99%//AF100757

C-HEMBB1001387

C-MAMMA1002317

C-MAMMA1002319

C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926

C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190

C-NT2RM1000242

C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028

C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE
D SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P
39942

C-NT2RM1000669

C-NT2RM1000781

C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798b
p//99%//AF092138

C-NT2RM1001008

C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//9
80bp//95%//AF085360

C-NT2RM1001074

C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239
aa//27%//

C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.
11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete

sequence.//0//1740bp//99%//AL031291

C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167

C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703

C-NT2RM2000032

C-NT2RM2000042

C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%//P50102

C-NT2RM2000093

C-NT2RM2000101

C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223

C-NT2RM2000192

C-NT2RM2000239

C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2e-314//1416bp//100%//AL080069

C-NT2RM2000259

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181aa//34%//P14918

C-NT2RM2000287

C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//AB020666

C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132

C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274

C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA

, partial cds.//0//1506bp//99%/U48251

C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.7E-68//419aa//36%/P50849

C-NT2RM2000374

C-NT2RM2000395

C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.6E-54//344aa//33%/P32802

C-NT2RM2000407

C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%/Q08469

C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//157aa//28%/P36113

C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.000089//377aa//24%/P22211

C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.8E-13//166aa//34%/P41823

C-NT2RM2000502

C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%/AF061243

C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//32%/P17437

C-NT2RM2000540

C-NT2RM2000567

C-NT2RM2000569

C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.7E-187//741aa//46%/P73505

C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%/D86987

C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%/P53973

C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487

C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//AF179221

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.4E-32//319aa//35%//Q08170

C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272

C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558

C-NT2RM2000639

C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576

C-NT2RM2000669

C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391

C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.8E-23//184aa//36%//Q15404

C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342

C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//P41877

C-NT2RM2000795

C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.5E-279//545aa//98%//P23514

C-NT2RM2000837

C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//AB015046

C-NT2RM2000952

C-NT2RM2000984

C-NT2RM2001004

C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//
Q60809

C-NT2RM2001065

C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.
//2.4E-15//266aa//26%//P46577

C-NT2RM2001131

C-NT2RM2001141

C-NT2RM2001152

C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp5
86G1822).//2.1E-293//1335bp//99%//AL080109

C-NT2RM2001194

C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//3
5%//P05143

C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//0.0
0000015//95aa//35%//P48724

C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP
10).//3.6E-10//177aa//32%//P97924

C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)
(L-GLUTAMINE AMIDOHYDROLASE).//1.3E-180//328aa//99%//P13264

C-NT2RM2001243

C-NT2RM2001247

C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166
//312aa//98%//P53995

C-NT2RM2001291

C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp56
4I052).//0//1694bp//99%//AL080063

C-NT2RM2001312

C-NT2RM2001319
C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584
C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00000002
9//334aa//22%//Q00808
C-NT2RM2001370
C-NT2RM2001393
C-NT2RM2001420
C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp5
86D0920).//0//1621bp//100%//AL050146
C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (
CAT2).//7.4E-121//437aa//57%//P52569
C-NT2RM2001504
C-NT2RM2001524
C-NT2RM2001544
C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.
3.4.1).//6.9E-27//90aa//42%//P38660
C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)
) (RO(SS-A)).//4.3E-61//312aa//44%//P19474
C-NT2RM2001582
C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0
//1000bp//100%//AB014610
C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692
C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0/
/2390bp//99%//AB007931
C-NT2RM2001930
C-NT2RM2001935
C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27
//216aa//34%//P28320
C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC RE

GION.//0.0000001//212aa//23%/P38250

C-NT2RM2001982

C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%/P37838

C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//28%/Q12730

C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%/Q09782

C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.000000029//83aa//44%/P40796

C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%/P46837

C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%/AB016789

C-NT2RM2002049

C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.0000099//338aa//24%/Q07878

C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%/Q61990

C-NT2RM2002091

C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840

C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%/AF030435

C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%/P49695

C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805

C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp4

34E0335).//0//1683bp//99%//AL117402
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2
 .7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167
 C-NT2RM4000061
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%//P52742
 C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%//X68101
 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//4.8E-13//
 686aa//23%//P25386
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439a
 a//41%//P16381
 C-NT2RM4000197
 C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0
 //1926bp//100%//AB018255
 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-11
 0) mRNA, complete cds.//1.1E-27//633bp//64%//L20303
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, comp
 lete cds.//2.2E-276//1124bp//97%//M99438
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1
 L.//0//2030bp//99%//AJ132637
 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%
 //AF083246
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21/
 /208aa//35%//Q24371
 C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//
 86%//AB025412
 C-NT2RM4000395
 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//17
 30bp//99%//AJ133769
 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I

./8E-20//393aa//24%/Q10297

C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete
cds.//0//2092bp//99%/AF097025

C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4
AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//
31%/P04280

C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%/P39955

C-NT2RM4000511

C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR
OTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%/P16884

C-NT2RM4000520

C-NT2RM4000585

C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box prote
in FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%/AF186273

C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0/
/1940bp//95%/AB014587

C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0
//1652bp//99%/AB020657

C-NT2RP1000040

C-NT2RP1000063

C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162b
p//99%/X98834

C-NT2RP1000101

C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%/P93471

C-NT2RP1000112

C-NT2RP1000124

C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//
60%/P51859

C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0

//1889bp//98%//AB023165

C-NT2RP1000170

C-NT2RP1000191

C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357

C-NT2RP1000243

C-NT2RP1000259

C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730

C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551

C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447

C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343

C-NT2RP1000357

C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%//AL080187

C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159

C-NT2RP1000416

C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423

C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257

C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580

C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653

C-NT2RP1000481

C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0

//2728bp//99%//D87686

C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020

C-NT2RP1000574//HOMEODOMAIN PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367

C-NT2RP1000581

C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233

C-NT2RP1000688

C-NT2RP1000695

C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379

C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434

C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//035566

C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960

C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223

C-NT2RP1000846

C-NT2RP1000851

C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//035566

C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823

C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.6E-105//504bp//99%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%
 //Q04652
 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete
 cds.//2.5E-236//966bp//99%//M17885
 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338
 C-NT2RP1000980
 C-NT2RP1000988
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mR
 NA, complete cds.//2.2E-78//1529bp//61%//L01790
 C-NT2RP1001014
 C-NT2RP1001395
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//
 67%//P91917
 C-NT2RP1001424
 C-NT2RP1001449
 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family pro
 tein (putative).//1.2E-137//629bp//100%//AJ005257
 C-NT2RP1001466
 C-NT2RP1001475
 C-NT2RP1001482
 C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1
 .6E-166//506aa//60%//P42803
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27)
 (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//03
 5566
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BE
 TA).//5.8E-121//271aa//89%//P47758

C-NT2RP1001616

C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594

C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40)
).//9.8E-17//79aa//55%//034136

C-NT2RP2000007

C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E
-177//726aa//47%//P51523

C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)
.//1.8E-22//184aa//34%//Q01730

C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol
og (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749

C-NT2RP2000054

C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3
.48) (R-PTP- EPSILON).//9.4E-16//45aa//100%//P49446

C-NT2RP2000067

C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN
).//3.4E-51//383aa//32%//P33450

C-NT2RP2000079

C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0/
/2286bp//100%//AB018338

C-NT2RP2000091

C-NT2RP2000097

C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//22
44bp//99%//AB018356

C-NT2RP2000120

C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117
//541aa//42%//P41877

C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0/
/2286bp//99%//AB023206

C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%/P35585

C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%/P41891

C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%/Q09329

C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%/AB023225

C-NT2RP2000173

C-NT2RP2000175

C-NT2RP2000195

C-NT2RP2000205

C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%/AB020699

C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%/P35568

C-NT2RP2000232

C-NT2RP2000233

C-NT2RP2000239

C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%/P56558

C-NT2RP2000270

C-NT2RP2000274

C-NT2RP2000283

C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//25%/Q10297

C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%/Q99676

C-NT2RP2000298

C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA
, complete cds.//4.3E-279//1193bp//99%//U82381

C-NT2RP2000328

C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760

C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.
//6.3E-115//674aa//46%//P17564

C-NT2RP2000369

C-NT2RP2000412

C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.
3E-228//415aa//100%//P52597

C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
complete cds.//0//1757bp//99%//AF102265

C-NT2RP2000438

C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844

C-NT2RP2000503

C-NT2RP2000510

C-NT2RP2000516

C-NT2RP2000603

C-NT2RP2000617

C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0/
/2482bp//99%//AB014514

C-NT2RP2000656

C-NT2RP2000658

C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E
-27//349aa//32%//Q01577

C-NT2RP2000704

C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA

LIGASE)//2.7E-100//488aa//44%/032038
 C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%/P12623
 C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0/
 /3347bp//99%/AB020680
 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.00
 0000056//179aa//29%/Q99104
 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//
 0.00000011//96aa//29%/P13466
 C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//
 28%/P26174
 C-NT2RP2000819
 C-NT2RP2000841
 C-NT2RP2000845
 C-NT2RP2000863
 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//
 99%/O60841
 C-NT2RP2000892
 C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244
 C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp56
 40043).//0//2487bp//99%/AL050390
 C-NT2RP2000938
 C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0
 //3458bp//99%/AB018298
 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//
 96%/AB024704
 C-NT2RP2000985
 C-NT2RP2001036
 C-NT2RP2001044
 C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0488.//0//2749bp//99%//AB007957

C-NT2RP2001065

C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5)
(PNP/PMP OXIDASE).//5.8E-46//222aa//45%//Q20939

C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%//P50232

C-NT2RP2001094

C-NT2RP2001119

C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ
132440

C-NT2RP2001218

C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHA
IN) (NMMHC).//2.2E-10//366aa//28%//P14105

C-NT2RP2001381

C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp43
4B174).//0//1495bp//100%//AL080146

C-NT2RP2001427

C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0/
/1748bp//99%//AB018340

C-NT2RP2001675

C-NT2RP2001721

C-NT2RP2001907

C-NT2RP2001969

C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA
, complete cds.//4.7E-177//1538bp//74%//AF062378

C-NT2RP2002046

C-NT2RP2002154

C-NT2RP2002208

C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%//P42568

C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16

521

C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//158bp//99%//AB015594

C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%//AF038958

C-NT2RP2002426

C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%//AB005289

C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%//Q11073

C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%//P12815

C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%//P55345

C-NT2RP2002621

C-NT2RP2002672

C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa//30%//O14345

C-NT2RP2002769

C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%//P29764

C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392

C-NT2RP2002954

C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669

C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P1012

9

C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190

C-NT2RP2003108

C-NT2RP2003117

C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.3E-82//642bp//68%//AF079765

C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%
//Q04652

C-NT2RP2003177

C-NT2RP2003194

C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580
bp//99%//AF151811

C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572

C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14/
/332aa//32%//P26337

C-NT2RP2003367

C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//
269aa//91%//P38378

C-NT2RP2003446

C-NT2RP2003533

C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1
.1.-).//1.7E-17//148aa//34%//P74261

C-NT2RP2003596

C-NT2RP2003629

C-NT2RP2003687

C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7
).//5.4E-29//85aa//72%//Q05481

C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (U

BIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%/P51669

C-NT2RP2003793

C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%/009175

C-NT2RP2003986

C-NT2RP2004042

C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%/AL096820

C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%/P38120

C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%/P36044

C-NT2RP2004463

C-NT2RP2004602

C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%/AB023139

C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%/AJ006291

C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa//33%/Q92355

C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%/Q10490

C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%/P53588

C-NT2RP2004802

C-NT2RP2004841

C-NT2RP2004936

C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%/P13692
C-NT2RP2004999
C-NT2RP2005000
C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0
//1694bp//99%/AB014515
C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%/AJ
011779
C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%/P32447
C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box
protein).//0//2388bp//98%/X98743
C-NT2RP2005140
C-NT2RP2005147
C-NT2RP2005159
C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete
cds.//0//2087bp//99%/AF097025
C-NT2RP2005270
C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cd
s.//0//2122bp//99%/D89053
C-NT2RP2005293
C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0/
/1515bp//99%/AB014576
C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protei
n MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%/AF072247
C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%/Q13823
C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI
NG FACTOR SRP75).//1.2E-13//185aa//38%/Q08170
C-NT2RP2005441
C-NT2RP2005453
C-NT2RP2005464

C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//
P38127

C-NT2RP2005472

C-NT2RP2005495

C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPH
A ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55
).//5.2E-81//166aa//88%//P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825
bp//99%//AF151803

C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mR
NA, complete cds.//0//3994bp//99%//AF092563

C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds.//2.4E-304//1
687bp//85%//AF035526

C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0
//2856bp//99%//AB007963

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGL
YOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTAS
E) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39
366

C-NT2RP2005555

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphat
e phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//145
5bp//98%//AF062085

C-NT2RP2005622

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).
//1E-11//128aa//36%//P47623

C-NT2RP2005637

C-NT2RP2005640

C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%/P5
6101

C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99
%/AJ010973

C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, co
mplete cds.//4.4E-200//908bp//99%/AF089814

C-NT2RP2005683

C-NT2RP2005690

C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0/
/1684bp//99%/AB018342

C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PR
OTEIN).//0.000000003//169aa//28%/P38074

C-NT2RP2005748

C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, c
omplete cds.//0//1968bp//99%/AF068868

C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, comple
te cds.//0//1966bp//99%/AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374a
a//38%/P47943

C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%/X90849

C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (
P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%/AF151351

C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEP
TIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP
) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%/Q
02038

C-NT2RP2005781

C-NT2RP2005804

C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%/P34223

C-NT2RP2005853
C-NT2RP2005868
C-NT2RP2005886
C-NT2RP2005890
C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0
//1977bp//99%//AB023188
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//
155aa//34%//P48837
C-NT2RP2006038
C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI
NG FACTOR SRP75).//1.5E-13//185aa//38%//Q08170
C-NT2RP2006052
C-NT2RP2006069
C-NT2RP2006071
C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp56
4B102).//0//1759bp//99%//AL049970
C-NT2RP2006106
C-NT2RP2006141
C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.
3E-189//899bp//97%//AB014554
C-NT2RP2006196
C-NT2RP2006200
C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%
//X96484
C-NT2RP2006237
C-NT2RP2006238
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN
LC1].//2E-59//388aa//32%//P46821
C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274

//1236bp//99%//AF035262

C-NT2RP2006333

C-NT2RP2006365

C-NT2RP2006393

C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEBOX).//0.00000034//50aa//50%//Q61658

C-NT2RP2006456

C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266

C-NT2RP2006467

C-NT2RP2006472

C-NT2RP2006565//Sus scrofa mRNA for SCAMP1 protein.//0//1276bp//84%//Y15710

C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYPIIG1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461

C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543

C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708

C-NT2RP3000072

C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164

C-NT2RP3000220

C-NT2RP3000251

C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334

C-NT2RP3000312

C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978

C-NT2RP3000333

C-NT2RP3000348

C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303.//0.000000028//185aa
//31%//025074

C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760

C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219

C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293

C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)///1.7E-139//679aa//41%//043143

C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185

C-NT2RP3000484

C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%//P28160

C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%//P15151

C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%//Q07283

C-NT2RP3000599

C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%//P51523

C-NT2RP3000644

C-NT2RP3000661

C-NT2RP3000665

C-NT2RP3000690

C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%//Q94650

C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%//

Q61982

C-NT2RP3000836

C-NT2RP3000841

C-NT2RP3000850

C-NT2RP3000852

C-NT2RP3000859

C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.9E-69//1611bp//61%//U53445

C-NT2RP3000869

C-NT2RP3000901

C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds.//0//3199bp//99%//AF064257

C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.7E-185//585bp//88%//AF015264

C-NT2RP3000980

C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159

C-NT2RP3001004

C-NT2RP3001081

C-NT2RP3001084

C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds./1.7E-94//787bp//66%//AF087433

C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%//P55201

C-NT2RP3001109

C-NT2RP3001116

C-NT2RP3001119

C-NT2RP3001133

C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%//AB018305

C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ
006266

C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REG
ION.//1.7E-10//196aa//27%//P53154

C-NT2RP3001214

C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0
000023//137aa//33%//P35663

C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.
11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%//P80193

C-NT2RP3001236

C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CO
NTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%//P14873

C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0
//2497bp//99%//AB020718

C-NT2RP3001307

C-NT2RP3001325

C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase ancho
ring protein 95, complete cds.//0//1213bp//99%//AB025905

C-NT2RP3001392

C-NT2RP3001396

C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%//P4
9711

C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009

C-NT2RP3001420

C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%//033529

C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%//
009053

C-NT2RP3001457

C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%//

P11632

C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1
475bp//99%//U13395

C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (T
RC8) mRNA, complete cds.//0//2295bp//99%//AF064801

C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%
//P20964

C-NT2RP3001621

C-NT2RP3001629

C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%//Q926
09

C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa//31%//O22468

C-NT2RP3001676

C-NT2RP3001679

C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa//27
%/P24733

C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa//30%
//Q04652

C-NT2RP3001896

C-NT2RP3001915

C-NT2RP3001929

C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%//P52742

C-NT2RP3004466

C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E
-113//466aa//42%//P34110

C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0/
/1520bp//99%//AB014532

C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0/
/974bp//95%//AB011126

C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHR
OID).//0.000000038//150aa//28%//Q01484

C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRN
A, complete cds.//0//1770bp//99%//AF026445

C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0
//1639bp//99%//AB007946

C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ
006266

C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%//Q02084

C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, comp
lete cds.//0//3972bp//98%//AF093097

C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEI
N).//1.7E-72//254aa//45%//P54352

C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%//P355
26

C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.9E-51//335aa//37%/
/Q64375

C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0
//3013bp//99%//AB020657

C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99
%//AB011538

C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568

C-NT2RP4000129

C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating
protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150

C-NT2RP4000151

C-NT2RP4000159

C-NT2RP4000185

C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0/
/4149bp//99%//AB014600

C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15
//104aa//40%//P15287

C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP
).//0//1932bp//99%//AJ006470

C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//2
08aa//76%//Q03173

C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa/
/43%//023968

C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.
//3.5E-297//1024aa//55%//P87115

C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
(ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631

C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).
//0.0000003//101aa//32%//P26372

C-NT2RP4000355

C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0
//4074bp//99%//AB018281

C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP)
mRNA, complete cds.//0//4782bp//99%//AF044195

C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).
//2.6E-77//262aa//54%//075570

C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.
n.//0//2412bp//99%//AJ238243

C-NT2RP4000381

C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738

C-NT2RP4000415

C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%/P45701

C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%/AL050078

C-NT2RP4000449

C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.//0.0000003//175aa//27%/P09309

C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%/P50101

C-NT2RP4000480

C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%/Q09475

C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%/P40484

C-NT2RP4000500

C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%/P45818

C-NT2RP4000524

C-NT2RP4000541

C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%/P40319

C-NT2RP4000560

C-NT2RP4000588

C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%/AF067730

C-NT2RP4000638

C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.//0.00000037//175aa//27%/P09309

C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.
1E-32//350aa//30%/P39625

C-NT2RP4000704

C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1
.1E-13//295aa//27%/Q11073

C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78
%/P10267

C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0/
/3392bp//95%/AB023148

C-NT2RP4000737

C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0
//3574bp//99%/AB023229

C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC RE
GION.//0.000000032//67aa//31%/P53915

C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0
//1927bp//99%/AB007939

C-NT2RP4000833

C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-9
4//810bp//65%/Y18265

C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//2
71aa//28%/Q00808

C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (
ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.7E-82//3
24aa//48%/009175

C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//
55%/P16415

C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%/03568

2

C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96/

/513aa//42%/P22314

C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROT
EIN).//2.6E-26//227aa//36%/Q06828

C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15
) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEAS
E DUB-1) (DEUBIQUITINATING ENZYME 1).//1.5E-76//346aa//43%/Q61068

C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%/Y16
521

C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014/
/185aa//25%/Q58900

C-NT2RP4000955

C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.
3.4.1).//1.4E-26//90aa//42%/P38660

C-NT2RP4000975

C-NT2RP4000979

C-NT2RP4000984

C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%/P34579

C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7
.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%/P70700

C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%/P39968

C-NT2RP4001006

C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0
//2482bp//99%/AB023181

C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T
RNA LIGASE)//1.5E-92//443aa//44%/Q09996

C-NT2RP4001057

C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%/
/Q64375

C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-

ATPASE).//1.3E-123//563aa//46%/P13586
 C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99
 %//AB023967
 C-NT2RP4001086
 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSR
 NA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%/P5
 1400
 C-NT2RP4001100
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115
 //224aa//100%/P38378
 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%/O15736
 C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%/Q07283
 C-NT2RP4001138
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SD
 AP).//0.00000021//93aa//33%/P44514
 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%/P33750
 C-NT2RP4001149
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM)
 (BRAVO).//3.4E-29//385aa//29%/P35331
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSO
 R (CTPT).//4.7E-29//227aa//35%/P52178
 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, com
 plete cds.//4.4E-104//1460bp//65%/U95760
 C-NT2RP4001207
 C-NT2RP4001210
 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.
 3.4.1).//6.2E-27//90aa//42%/P38660
 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43
 %//Q04652

C-NT2RP4001235

C-NT2RP4001256

C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0/
/2876bp//99%//AB020682

C-NT2RP4001274//Human transporter protein (gl7) mRNA, complete cds.//4.4
E-58//1196bp//61%//U49082

C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%//Q07283

C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTE
IN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%/
/P24391

C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5
.//8.5E-213//1129bp//92%//AJ001119

C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp/
/99%//AJ007014

C-NT2RP4001343

C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL)
, complete cds.//2.7e-310//1400bp//100%//AB017494

C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain ho
molog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%//U53445

C-NT2RP4001353

C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PRO
TEIN).//1.6E-19//222aa//30%//Q08180

C-NT2RP4001373

C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112
) (TYROSINE- PROTEIN KINASE 1).//9.2E-17//146aa//35%//P18160

C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//
2E-53//436aa//30%//Q10085

C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0
//2716bp//99%//AB023140

C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%/Q141
41

C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54
%/Q99676

C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, compl
ete cds.//2.7E-66//738bp//71%/AF129131

C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC
1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%/Q02218

C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//2
9%/P39010

C-NT2RP4001502

C-NT2RP4001507

C-NT2RP4001524

C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENI
C REGION.//5.7E-54//242aa//38%/P25656

C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation
factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%/AF1529
61

C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa
//24%/P96902

C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//
26%/Q02453

C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%/P35197

C-NT2RP4001571

C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds./
/0//3046bp//99%/AF100756

C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%
//AJ223830

C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA

LIGASE) (ILERS).//1.7E-141//373aa//47%/P73505
 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0/
 /1897bp//99%/AB020676
 C-NT2RP4001614
 C-NT2RP4001634
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//
 234aa//32%/P40469
 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-1
 9//111aa//45%/P25323
 C-NT2RP4001677
 C-NT2RP4001679
 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
 SUBUNIT (CPSF 100 KD SUBUNIT).//4E-10//243aa//25%/Q10568
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10/
 /128aa//32%/Q10282
 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%/Q09332
 C-NT2RP4001739
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E
 -236//665aa//58%/P51523
 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%/P98174
 C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0
 //3144bp//99%/AB023232
 C-NT2RP4001803
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27)
 (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%/03
 5566
 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//5

4%/P55083

C-NT2RP4001828

C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.
//6.3E-99//555bp//73%//AF155595

C-NT2RP4001861//TRICHOHYALIN.//1E-35//307aa//34%//P37709

C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp56
40043).//0//1306bp//98%//AL050390

C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00000001
4//345aa//25%//Q00808

C-NT2RP4001901

C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32
%//Q12024

C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P4
9711

C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77)
(PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPART
YL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
./1.5E-13//211aa//28%//Q43209

C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//2
7%//P13816

C-NT2RP4001953

C-NT2RP4001966

C-NT2RP4001975

C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%
//Q04652

C-NT2RP4002052

C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX
PROTEIN 13)///1E-137//679aa//40%//043143

C-NT2RP4002071

C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)
).//3E-150//722aa//39%/Q05481

C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAIN
S (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//3
1%/P52655

C-NT2RP4002298

C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%/P38938

C-NT2RP4002791

C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434F172 (from clone DKFZp43
4F172).//0//2557bp//99%/AL080202

C-NT2RP4002905

C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%/P53552

C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//2
80aa//27%/Q00808

C-NT2RP5003492

C-NT2RP5003500

C-NT2RP5003506

C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3
E-23//219aa//40%/P37116

C-NT2RP5003524

C-NT2RP5003534

C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%/P02262

C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000
042//102aa//32%/O14727

C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//
1393bp//97%/AF058922

C-OVARC1000035

C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (R

NASE LE).//0.00000032//60aa//45%/P80022
 C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%/Q02874
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1
) (VCAF) (CFF).//8.4E-14//259aa//30%/P51610
 C-OVARC1000113
 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562
 bp//99%/AF132955
 C-OVARC1000148
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 inter
 acting with transcription factor Spl.//2.5E-95//461bp//98%/AJ242975
 C-OVARC1000168
 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, comple
 te cds.//1.8E-32//511bp//65%/AF068332
 C-OVARC1000212
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INT
 ERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-1
 20//351aa//54%/Q16665
 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLY
 PEPTIDASE) (LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III) (AMINO
 PEPTIDASE YSCI).//5.4E-53//384aa//30%/P14904
 C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%/P23249
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%/P
 29363
 C-OVARC1000321
 C-OVARC1000326
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REG
 ION.//5.9E-14//200aa//27%/P40004
 C-OVARC1000347
 C-OVARC1000384

C-OVARC1000411
C-OVARC1000420
C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205
C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//99%//AL080126
C-OVARC1000461
C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075
C-OVARC1000466
C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452
C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636
C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91%//AF051850
C-OVARC1000564
C-OVARC1000576
C-OVARC1000588
C-OVARC1000605
C-OVARC1000640
C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%//D43772
C-OVARC1000661
C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886
C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q5834
3
C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533

C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%
 //AJ130978
 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215/
 /1027bp//98%//AF132946
 C-OVARC1001162
 C-OVARC1001243
 C-OVARC1001296
 C-OVARC1001360
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involve
 d in B-CLL.//6E-148//683bp//99%//AJ224819
 C-OVARC1001425
 C-PLACE1000005
 C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%//P53538
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONAS
 E).//2.8E-29//134aa//43%//P52046
 C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5
 .5e-312//1411bp//99%//AB020639
 C-PLACE1000185
 C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0
 //1904bp//99%//AB023194
 C-PLACE1000347
 C-PLACE1000374
 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0/
 /2208bp//99%//AB020660
 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ2
 24979
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30/
 /352aa//31%//P15151
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//

72%/P23246

C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//0.0000028//134aa//29%/P53368

C-PLACE1000435

C-PLACE1000444

C-PLACE1000562

C-PLACE1000564

C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE- BINDING PROTEIN 1).//1.6E-270//437aa//86%/P32455

C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%/AB020657

C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%/AF044201

C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%/Q08891

C-PLACE1000716

C-PLACE1000748

C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.6E-250//1189bp//97%/AB028449

C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%/AB014548

C-PLACE1000798

C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.5E-49//181aa//54%/P32899

C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%/P39010

C-PLACE1000948

C-PLACE1000972

C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%/Q03070

C-PLACE1001000

C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//150
0bp//99%//AF065485

C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%
//Q04652

C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FING
ER PROTEIN REQUIEM).//3E-33//138aa//42%//Q61103

C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8./
/2.3E-61//132aa//46%//Q12929

C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete
sequence.//0//2118bp//99%//AC005412

C-PLACE1001412

C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT S
EQUENCE, in unordered pieces.//0//1440bp//99%//AL031660

C-PLACE1001503

C-PLACE1001570

C-PLACE1001610

C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (E
C 3.1.2.14) (THIOESTERASE II).//4E-81//263aa//56%//P08635

C-PLACE1001729

C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//3.5E-75//439a
a//41%//P16381

C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63
//427aa//35%//Q57290

C-PLACE1001810

C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta s
ubunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953

C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524

C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0

//1196bp//99%//AF131737

C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//
1729bp//99%//AF099935

C-PLACE1001928

C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49
091

C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211

C-PLACE1002072

C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
(ADENYLYL CYCLASE).//0.00000053//188aa//29%//P49606

C-PLACE1002140

C-PLACE1002163

C-PLACE1002170

C-PLACE1002433

C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133
aa//29%//Q13105

C-PLACE1002465

C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.
7E-214//956bp//94%//AB018256

C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternativ
ely spliced, complete cds.//0//1750bp//99%//AF068180

C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//30
5aa//33%//Q15391

C-PLACE1002794

C-PLACE1002815

C-PLACE1002839

C-PLACE1002851

C-PLACE1002941

C-PLACE1002996

C-PLACE1003045

C-PLACE1003092

C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268

C-PLACE1003108

C-PLACE1003145

C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743

C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750

C-PLACE1003200

C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//99%//AL080133

C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//P51522

C-PLACE1003334

C-PLACE1003342

C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715

C-PLACE1003369

C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200

C-PLACE1003611

C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824

C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//209aa//34%//Q08170

C-PLACE1003711

C-PLACE1003723

C-PLACE1003762

C-PLACE1003771

C-PLACE1003784

C-PLACE1003923

C-PLACE1003936

C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK G
AMMA-1 CHAIN).//2.4E-124//326aa//73%//P80385

C-PLACE1004104

C-PLACE1004114

C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANS
DUCIN BETA CHAIN 4).//6.1E-181//340aa//96%//P29387

C-PLACE1004149

C-PLACE1004156

C-PLACE1004161

C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ0
10071

C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%//Q6255
6

C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precu
sor, mRNA, complete cds.//0//1882bp//99%//AF069493

C-PLACE1004258

C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36
//389aa//31%//015393

C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, c
omplete cds.//0//1498bp//99%//AF084830

C-PLACE1004289

C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750

C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767b
p//99%//Y11588

C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1

mRNA, complete cds.//0//2512bp//99%//AF100153
C-PLACE1004376
C-PLACE1004388
C-PLACE1004405
C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33
%/Q63448
C-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subuni
t precursor, mRNA, nuclear gene encoding mitochondrial protein, complete
cds.//0//985bp//99%//U49283
C-PLACE1004451
C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823
C-PLACE1004473
C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRN
A, complete//1.3E-209//954bp//99%//AF026445
C-PLACE1004516
C-PLACE1004548
C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568
C-PLACE1004629//PROTEIN OS-9-PRECURSOR.//7.7E-18//264aa//32%//Q13438
C-PLACE1004645
C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane re
ceptor p63.//4.4E-42//985bp//59%//X66277
C-PLACE1004664
C-PLACE1004672
C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257)
./1.6E-95//191aa//96%//P12815
C-PLACE1004691
C-PLACE1004722
C-PLACE1004736

C-PLACE1004740

C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LI
GASE E3 COMPONENT) (N- RECOGNIN).//4.4E-35//578aa//27%/060152

C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal
VI, complete cds.//7.1E-224//790bp//98%/AB022918

C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAE
RIN).//1.9E-32//259aa//32%/P30337

C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
(ADENYLYL CYCLASE).//4.7E-65//695aa//29%/Q01631

C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI
NG FACTOR SRP75).//5.9E-19//196aa//36%/Q08170

C-PLACE1004824

C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%/Q08891

C-PLACE1004885

C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI
CASE SPAC10F6.02C.//9.3E-11//94aa//47%/042643

C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//
4.9E-48//198aa//44%/P06151

C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1
853bp//98%/AF099936

C-PLACE1004934

C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%/Q93794

C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2
E-14//205aa//26%/Q11073

C-PLACE1004982

C-PLACE1005026

C-PLACE1005027

C-PLACE1005046

C-PLACE1005077

C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209
 //1031bp//96%//L40401

C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%
 //Q04652

C-PLACE1005111

C-PLACE1005181

C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636

C-PLACE1005206

C-PLACE1005232

C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E
 -27//349aa//32%//Q01577

C-PLACE1005261

C-PLACE1005266

C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.
 2E-297//1341bp//100%//AB011182

C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%/
 /P53352

C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (
 AK3).//2E-111//226aa//92%//P08760

C-PLACE1005308

C-PLACE1005313

C-PLACE1005327

C-PLACE1005335

C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDO
 URIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL
 HYDROLYASE).//8.6E-09//194aa//27%//033335

C-PLACE1005374

C-PLACE1005480

C-PLACE1005481

C-PLACE1005494//Homo sapiens mRNA for transient receptor potential prote
in TRP6.//0//1649bp//99%//AJ006276

C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.
//5.6E-52//173aa//57%//Q09251

C-PLACE1005550

C-PLACE1005554

C-PLACE1005623

C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete
cds.//0//2130bp//99%//AF083255

C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4
.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350

C-PLACE1005730

C-PLACE1005755

C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (E
C 3.1.2.14) (THIOESTERASE II).//2.5E-79//209aa//53%//P08635

C-PLACE1005803

C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
.//1.1E-217//994bp//99%//AF027156

C-PLACE1005851

C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120

C-PLACE1005923

C-PLACE1005925

C-PLACE1005934

C-PLACE1005936

C-PLACE1005951

C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//
37%//P43636

C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLY
PEPTIDASE)//5.4E-54//455aa//32%//P14904

C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAF II-90).//0.00000014//254aa//25%//P38129

C-PLACE1005990

C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876

C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906

C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//AF039023

C-PLACE1006139

C-PLACE1006159

C-PLACE1006167

C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706

C-PLACE1006195

C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747

C-PLACE1006225

C-PLACE1006236

C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//P28675

C-PLACE1006246

C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//1271bp//99%//AL080066

C-PLACE1006335

C-PLACE1006357

C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085

C-PLACE1006412

C-PLACE1006414
 C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%/P49910
 C-PLACE1006445
 C-PLACE1006470
 C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%/Q90595
 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%/Q00004
 C-PLACE1006492
 C-PLACE1006531
 C-PLACE1006552
 C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//2182bp//99%/AC007383
 C-PLACE1006615
 C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%/AB023145
 C-PLACE1006673
 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//734bp//62%/AB015630
 C-PLACE1006704
 C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%/Q59263
 C-PLACE1006782
 C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%/P08547
 C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%/P35123

C-PLACE1006883

C-PLACE1006901

C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181

C-PLACE1006932

C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//
6.7E-48//278aa//41%//Q10000

C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P9799
8

C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete
cds.//0//1770bp//99%//AB023421

C-PLACE1006961

C-PLACE1006962

C-PLACE1006966

C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PR
OTEIN 12) (DER12).//3.2E-35//180aa//33%//Q14542

C-PLACE1007021

C-PLACE1007105

C-PLACE1007178

C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDA
SE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370a
a//31%//P54304

C-PLACE1007238

C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-
II, hS-II-T1, complete cds.//6.5E-216//1068bp//96%//D50495

C-PLACE1007242

C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%//P34579

C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//
Y15908

C-PLACE1007274

C-PLACE1007282

C-PLACE1007301

C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%//AF117649

C-PLACE1007342

C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870

C-PLACE1007367

C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715

C-PLACE1007386

C-PLACE1007402

C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%//Q17320

C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%//P27487

C-PLACE1007450

C-PLACE1007452

C-PLACE1007460

C-PLACE1007484

C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%//P52734

C-PLACE1007507

C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%//P08728

C-PLACE1007524

C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164

C-PLACE1007544

C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III./
/1E-49//361aa//36%/P34537

C-PLACE1007583

C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44
%/Q99676

C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0
//713bp//99%/AB023194

C-PLACE1007621

C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%/P
32506

C-PLACE1007645

C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0
//1952bp//99%/AB023194

C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGE
N HOMOLOG).//8.7E-09//279aa//28%/Q26457

C-PLACE1007690

C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%/P43535

C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.
//0//3431bp//99%/AF061243

C-PLACE1007725

C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231
aa//42%/P10265

C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9
.2E-294//1504bp//94%/AB014585

C-PLACE1007746

C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%
/AB019602

C-PLACE1007810

C-PLACE1007843

C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region
, segment 3/13.//0//1751bp//99%//AP000010

C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0
//3112bp//99%//AB018309

C-PLACE1007897

C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN
II).//2.6E-14//370aa//25%//Q99323

C-PLACE1007954

C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, com
plete cds.//0//2252bp//99%//AF084530

C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds.//0//2300bp//99%//AF079529

C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.
1E-36//202aa//48%//P52272

C-PLACE1007990

C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110)
(SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622

C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4
unordered pieces.//0//1833bp//99%//AC005628

C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107)
(107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590

C-PLACE1008095

C-PLACE1008122

C-PLACE1008129

C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.
//1.3E-24//395aa//31%//Q09531

C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%//P37709

C-PLACE1008209

C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).
//1.3E-283//671aa//77%/P53620
C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//3
7%/P12689
C-PLACE1008280
C-PLACE1008309
C-PLACE1008329
C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0/
/1853bp//100%/AB014579
C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%/P05432
C-PLACE1008401
C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS AS
SOCIATED PROTEIN) (TAP).//0//698aa//95%/P41541
C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%/Q06527
C-PLACE1008457
C-PLACE1008465
C-PLACE1008488
C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1
-21.1. Contains part of a gene for a novel protein with ZU5 domain simil
ar to part of Tight Junction Protein Z01 (TJP1) and UNC5 Homologs, the g
ene for a novel BZRP (peripheral benzodiazapine recepto//0//1980bp//99%/
/AL031778
C-PLACE1008531
C-PLACE1008532
C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIG
EN).//1.1E-09//62aa//48%/P22620
C-PLACE1008568
C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155).
(155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%/P37199

C-PLACE1008621

C-PLACE1008626

C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp/
/99%//AJ006591

C-PLACE1008629

C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//AF044333

C-PLACE1008693

C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406

C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//035345

C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1 A.//2.3E-269//1225bp//99%//AJ004974

C-PLACE1008813

C-PLACE1008854

C-PLACE1008867

C-PLACE1008887

C-PLACE1008902

C-PLACE1008925

C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623

C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112

C-PLACE1009045

C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582

C-PLACE1009090

C-PLACE1009091

C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2)

./1.9E-44//480aa//30%/P30432

C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT)./1.1E-179//452aa//67%
//P51814

C-PLACE1009110

C-PLACE1009111

C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PRO
TEIN-ASSOCIATED PROTEIN E6-AP)./2E-68//181aa//43%/Q05086

C-PLACE1009158

C-PLACE1009166

C-PLACE1009174

C-PLACE1009186

C-PLACE1009190

C-PLACE1009230

C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, c
omplete cds; nuclear gene for mitochondrial product./2.1E-132//1229bp//
75%/AF107295

C-PLACE1009328

C-PLACE1009335

C-PLACE1009338

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2./2.5E-10//151aa//29%/Q12
067

C-PLACE1009375

C-PLACE1009388

C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.
//0.000000047//165aa//33%/Q09820

C-PLACE1009434

C-PLACE1009443

C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-K
INASE) (PTDINS-4-KINASE) (PI4K-ALPHA)./7.8E-71//82aa//89%/P42356

C-PLACE1009459
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//
 550aa//93%//P54319
 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSO
 ME III.//3.9E-40//179aa//37%//P34580
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF E
 XCHANGE FACTOR).//8.1E-99//228aa//75%//Q99418
 C-PLACE1009542
 C-PLACE1009571
 C-PLACE1009581
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//2
 91aa//40%//Q00808
 C-PLACE1009607
 C-PLACE1009621
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P
 25159
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.5E-
 285//538aa//99%//P55161
 C-PLACE1009665
 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp
 //100%//AF062534
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN
 C12G12.13C IN CHROMOSOME I.//7E-33//166aa//43%//Q09876
 C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200
 C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, com
 plete cds.//4.3E-294//1329bp//100%//AB012190
 C-PLACE1009794
 C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0

//2685bp//99%//AB020712

C-PLACE1009886

C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENI
C REGION.//1.9E-108//277aa//43%//P53145

C-PLACE1009971

C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6
E-59//450aa//34%//P28175

C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp56
40123).//0//1962bp//99%//AL080122

C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mR
NA, complete cds.//5.2E-70//736bp//73%//U48288

C-PLACE1010023

C-PLACE1010031

C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1
402bp//94%//X84692

C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./
/0//2019bp//99%//AF065482

C-PLACE1010076

C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q626
71

C-PLACE1010102

C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44
%//Q04652

C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp5
86M1418).//0//1974bp//99%//AL049385

C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX C
OMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRAN
SCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082

C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//43

1aa//23%/P35662

C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%/Q01130

C-PLACE1010202

C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%/P25722

C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%/AL080122

C-PLACE1010293

C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.1E-09//350aa//22%/P52178

C-PLACE1010324

C-PLACE1010329

C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.00000002//126aa//29%/P34024

C-PLACE1010364

C-PLACE1010383

C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%/AB020643

C-PLACE1010491

C-PLACE1010492

C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%/AB022718

C-PLACE1010529

C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.00000012//616aa//24%/P25386

C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor

protein, complete cds.//0//1904bp//99%//AB017546
 C-PLACE1010616
 C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016/
 /120aa//28%//P02642
 C-PLACE1010629
 C-PLACE1010630
 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01
 755
 C-PLACE1010714
 C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-
 C, complete cds.//4E-299//1091bp//99%//AB019987
 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, par
 tial cds.//8.9E-91//668bp//82%//AF020267
 C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061
 C-PLACE1010786
 C-PLACE1010800
 C-PLACE1010811
 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7
).//1.3E-143//407aa//58%//Q05481
 C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0/
 /1885bp//99%//AB011182
 C-PLACE1010900
 C-PLACE20000050
 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH
 PROTEIN).//2.4E-191//828aa//48%//P21783
 C-PLACE4000590
 C-PLACE4000638
 C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17
 //201aa//34%//P49816

C-Y79AA1001647

【 0 8 3 0 】

相同性検索結果データ 7.

実施例 1 6 で選抜した54クローンの5'末端クローン配列に対するSwissProt相同性検索結果データ

各データは、クローン配列名、トップヒットデータのDefinition、P値:比較配列の長さ (base):相同性(%）、トップヒットデータのOrganism、トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)./
/0.13//52//38//P25860

F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15)
(UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64
E) (DEUBIQUITINATING ENZYME 64E).//2.2e-28//104//59//Q24574

F-HEMBA1003854//VERPROLIN.//0.012//138//31//P37370

F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FR
AGMENT).//0.93//39//33//Q37131

F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).
//0.90//20//50//P38524

F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16).//7.6e-46//141//58//Q15
973

F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT).//0.0033//32//46/
/P70560

F-HEMBA1006092//VERPROLIN.//1.0//62//35//P37370

F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10).//0.30/
/41//36//P12350

F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.089//21//52/
/Q02593

F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).//0.38

//156//30//P28697

F-HEMBB1000672

F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0//30//36//P16
012

F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S
1).//3.7e-54//241//47//P47853

F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3' REGION (ORF3).//0.
59//48//39//Q51483

F-MAMMA1002094

F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.26//58
//27//P06333

F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS
E DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III
) (FRAGMENT).//8.9e-20//83//48//P10895

F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT).//1.0//42//40//P19326

F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID
LABILE CHAIN PRECURSOR (ALS).//6.0e-23//207//32//Q02833

F-NT2RM4001178//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.012//156//28//Q90267

F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0012//81//37//P.
13816

F-NT2RP2000198//CREB-BINDING PROTEIN.//0.29//98//37//Q92793

F-NT2RP2000551//PROTEIN Q300.//0.00017//23//60//Q02722

F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401.//1.0//41//29//Q57844

F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.27//13//61//Q016
44

F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-).//0.089//99//29//Q990
14

F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAG
MENT).//4.0e-13//177//28//P16372

F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//0.37//12
//75//P53820

F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)./
/0.99//61//32//Q42616

F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2.//3.3e-10//90//35//Q06666

F-NT2RP2002843//CYTOCHROME B.//0.78//103//26//P48884

F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG.//0.40//28//46//
P37209

F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1.//0.80//55//32//P81303

F-NT2RP2004095

F-NT2RP2004732

F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.18//18//55
//Q48251

F-NT2RP2005454

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A
DENYLYLTRANSFERASE) (FRAGMENT).//7.4e-38//136//41//P51003

F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180
//28//P32323

F-NT2RP2005882

F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//3
9//P39217

F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULA
TORY PROTEIN ALGR3).//0.00035//127//31//P15276

F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P0
5204

F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX
-1) (FRAGMENT).//0.064//110//34//P39881

F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA
GMENT).//0.020//95//29//P15583

F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.
8e-05//165//29//P17437

F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P
EPTIDE P-D] (FRAGMENT).//0.035//152//30//P10162

F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEI
N).//0.38//124//31//P28284

F-OVARC1001029

F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377

F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN)
(IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35)
(CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845

F-PLACE1005549//RH01 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRE
SSOR SKC1).//3.2e-08//205//24//P53046

F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P0
1668

【 0 8 3 1 】

相同性検索結果データ 8.

実施例 1 6 で選抜した 54 クロンの 5' 末端クローン配列に対する EST と STS を除
いた GenBank 相同性検索結果データ

各データは、クローン配列名、トップヒットデータの Definition、P 値: 比較配
列の長さ (base): 相同性 (%), トップヒットデータの Accession No. の順に // で区
切って記載した。

なお、相同性のスコアの P 値が 1 より大であった場合はデータは示さない。

F-HEMBA1000497

F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, L
eu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710

F-HEMBA1003854//Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS
***, 18 unordered pieces.//1.7e-05//412//61//AC005081

F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//

0.77//466//59//AC002386

F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt] .//2.9e-47//341//77//S54641

F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851

F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738

F-HEMBA1006406//HS_2268_B2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566

F-HEMBA1006650//H.sapiens CpG island DNA genomic MseI fragment, clone 5h5, forward read cpg5h5.fl1a.//9.4e-24//143//96//Z55730

F-HEMBA1006812//X.laevis xUBFalpha1 mRNA for upstream binding factor 2.//0.96//234//64//X59863

F-HEMBB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158

F-HEMBB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760

F-HEMBB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127

F-MAMMA1001252

F-MAMMA1002094//H.sapiens CpG island DNA genomic MseI fragment, clone 184g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993

F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136

F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//24

5//61//D42108

F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199

F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961

F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411

F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//0.00013//121//76//AC005670

F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827

F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812

F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622

F-NT2RP2001214

F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189

F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589

F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094

F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10 q25, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.//0.032//141//70//AC006097

F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.//1.8e-22//377//69//AP000018

F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050

F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476

F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233

F-NT2RP2004095//HS_3083_A1_A02_MF CIT Approved Human Genomic Spermlibrary D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698

F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035

F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970

F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410

F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770

F-NT2RP2005806//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652

F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242

F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775

F-NT2RP3001723//H.sapiens CpG island DNA genomic MseI fragment, clone 13g5, reverse read cpg13g5.rtl1a.//2.2e-18//163//85//Z56771

F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296_K_1, complete sequence.//1.3e-76//351//86//AC005180

F-NT2RP3003155

F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//140055

F-OVARC1000008////0.0040//674//57//M82836

F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3

for transcriptional activator IE175 (= ICP 4).//1.1e-07//519//59//X06461
F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221

F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769

F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427

F-PLACE1003030

F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081

F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//3.1e-39//214//98//AL031660

【 0 8 3 2 】

相同性検索結果データ 9.

実施例 1 6 で選抜した54クローンの3'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ

各データは、クローン配列名、トップヒットデータのDefinition、P値:比較配列の長さ (base):相同性(%), トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

R-HEMBA1000497//***ALU WARNING: Human Alu-J subfamily consensus sequence .//1.4e-38//185//84//U14567

R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785

R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene

for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, ST
 Ss, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL03128
 1

R-HEMBA1004193//***ALU WARNING: Human Alu-J subfamily consensus sequence
 .//1.1e-34//188//81//U14567

R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Canc
 er Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC
 004241

R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complet
 e sequence.//3.1e-21//341//67//AJ010598

R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequ
 ence.//1.7e-24//307//71//AC004678

R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cy
 clase.//0.76//246//62//X63282

R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.2
 2-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an
 STS, complete sequence.//1.3e-31//297//77//AL023574

R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, compl
 ete sequence.//1.8e-15//350//65//AC003071

R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCI
 NG IN PROGRESS ***, in unordered pieces.//1.8e-55//430//81//Z82207

R-HEMBB1000672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequ
 ence.//9.1e-39//437//71//AC006166

R-HEMBB1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete
 sequence.//1.5e-37//275//85//AC004593

R-HEMBB1001871//Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUE
 NCING IN PROGRESS ***, 5 unordered pieces.//0.00097//410//59//AC004688

R-MAMMA1001252//Homo sapiens clone 201104, *** SEQUENCING IN PROGRESS **
 *, 4 unordered pieces.//2.9e-13//364//64//AC004529

R-MAMMA1002094//HS_3163_A1_A09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1.6e-21//283//73//AC005258

R-NT2RM4000657

R-NT2RM4000783

R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073

R-NT2RM4001178

R-NT2RM4002420

R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 complete genomic sequence, complete sequence.//0.58//108//67//AC002307

R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//D30043

R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//0.0058//166//69//AC005324

R-NT2RP2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Varlp (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822

R-NT2RP2001460

R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228

R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome X p11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181

R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168

R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DX

S366 and DXS87 on chromosome X *./5.3e-39//449//72//Z81014

R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence./0.0097//498//59//AC005412

R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey sequence./1.2e-32//344//75//AQ196754

R-NT2RP2003799///3.6e-05//408//60//AL010237

R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces./2.1e-10//455//61//AL034557

R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GS Ss, complete sequence./5.1e-51//383//74//AL031287

R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), c complete sequence./0.062//315//61//AC005219

R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments./0.75//246//63//Z86062

R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence./0.91//232//61//AC005232

R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, c complete sequence./1.3e-19//405//66//U37368

R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence./1.1e-09//533//60//Z97348

R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence./0.00026//499//58//AL034560

R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence./0.00035//337//61//AC002466

R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296_K_1, complete sequence./1.8e-44//307//86//AC005180

R-NT2RP3003155

R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6,
genomic survey sequence.//0.95//95//65//B21351

R-OVARC1000008

R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequ
ence.//0.91//83//71//AC005161

R-OVARC1000751//HS_2222_A2_C09_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2222 Col=18 Row=E, genomic survey
sequence.//2.8e-12//176//72//AQ033143

R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore
X library) and PAC RPC11-93D11 (from Roswell Park Cancer Center) comple
te sequence.//1.2e-09//165//75//AC002357

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete
sequence.//6.2e-52//514//75//AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subu
nit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387

R-PLACE1005549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon
e: K19P17, complete sequence.//0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, *** SEQUENC
ING IN PROGRESS ***, in unordered pieces.//1.1e-88//497//91//AL031660

【 0 8 3 3 】

相同性検索結果データ 1 0.

実施例 1 6 で選抜した54クローンの5'末端クローン配列に対するHuman Unigen
e相同性検索結果データ

各データは、クローン配列名、トップヒットデータのTitle、P値:比較配列の
長さ (base):相同性(%)、トップヒットデータのAccession No.の順に//で区切っ
て記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000497//ou15a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone I
MAGE:1626332 3', mRNA sequence.//1.0//186//65//AI018130

F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element;, mRNA sequence.//3.7e-06//140//70//AA749151

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt] .//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//AB000732

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element;, mRNA sequence.//0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:002710 002710 GAG POLYPROTEIN. ;, mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087

F-HEMBA1006812//zh49f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415417 3', mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBA1000672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBA1001197//tq45e03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:001940 001940 STRAWBERRY NOTCH ;, mRNA sequence.//1.2e-16//117//92//AI580023

F-HEMBA1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

F-NT2RM4000634//DKFZp434D1813_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence.//1.8e-20//470//65//AI703299

F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876

F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//L11329

F-NT2RM4002420//wg39f11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367501 3' similar to contains element L1 L1 repetitive element ;, mRNA sequence.//1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997

F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence.//5.0e-07//116//71//AA017066

F-NT2RP2000660//qx01g11.x1 NCI_CGAP_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence.//0.027//120//65//AI225283

F-NT2RP2001214

F-NT2RP2001460//wb50h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence.//0.0013//89//78//AI651878

F-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ;, mRNA sequence.//2.3e-18//120//93//AA427992

F-NT2RP2002056//tw44g09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element; , mRNA sequence.//2.

4e-07//99//79//AI811687

F-NT2RP2002677

F-NT2RP2002755//zj83d10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461491 3' similar to contains element TAR1 repetitive element ;, mRNA sequence.//1.9e-19//229//76//AA705059

F-NT2RP2002843//wt88d12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR:P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN. ;, mRNA sequence.//8.2e-15//314//67//AI964055

F-NT2RP2003101//wi65a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence.//0.38//106//68//AI763133

F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979

F-NT2RP2004095

F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691

F-NT2RP2004920//wz68d10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR:000172 000172 LINE-1 REVERSE TRANSCRIPTASE ;, mRNA sequence.//0.0020//220//61//AI969546

F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194

F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770

F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mRNA sequence.//2.0e-05//385//62//Z78328

F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362

F-NT2RP3001282

F-NT2RP3001723//ws73d05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSR1.t1 TAR1 TAR1 repetitive element ;, mRNA sequence.//2.6e-07//245//66//AW008782

F-NT2RP3002099//yg49d01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence.//0.58//164//64//R46086

F-NT2RP3003155

F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997

F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565

F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541

F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802

F-OVARC1001029//qv29c05.x1 NCI_CGAP_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element ;, mRNA sequence.//0.0012//145//68//AI252422

F-PLACE1000814//ak42f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence.//7.1e-31//275//76//AA868469

F-PLACE1003030

F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//1.2e-57//737//67//AJ010046

F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence.//2.2e-21//216//76//H52716

【 0 8 3 4 】

相同性検索結果データ 1 1.

実施例 1 6 で選抜した54クローンの3'末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、クローン配列名、トップヒットデータのTitle、P値:比較配列の長さ (base):相同性(%）、トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないも

のは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

R-HEMBA1000497//np09h02.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains Alu repetitive element;contains element MER22 repetitive element ;, mRNA sequence.//6.2e-38//185//83//AA614254

R-HEMBA1001750//yy71b10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278971 3', mRNA sequence.//0.0045//193//63//N63303

R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310//80//AL049263

R-HEMBA1004193//tr01e08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.//1.5e-33//186//81//AI914747

R-HEMBA1004860//qh16b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA sequence.//0.017//118//69//AI218308

R-HEMBA1005572//wj16h05.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA sequence.//4.6e-111//522//99//AI861830

R-HEMBA1006038//DKFZp434E1117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5', mRNA sequence.//1.2e-22//295//72//AL041450

R-HEMBA1006092//qt30d09.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1949489 3' similar to contains element PTR5 repetitive element ;, mRNA sequence.//1.4e-87//422//98//AI337963

R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291//76//AB018295

R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK./3.6e-09//319//62//X97630

R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087

R-HEMBA1000672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//74//AL096734

R-HEMBB1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar to contains Alu repetitive element;, mRNA sequence.//9.9e-44//275//88//AA410788

R-HEMBB1001871//wg20c02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321

R-MAMMA1001252//aa61h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to contains Alu repetitive element;contains element XTR repetitive element ;, mRNA sequence.//9.0e-19//127//91//AA504355

R-MAMMA1002094//wd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mRNA sequence.//2.5e-68//328//99//AI936520

R-NT2RM4000634//DKFZp434F2016_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3', mRNA sequence.//8.2e-20//185//81//AL041146

R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992

R-NT2RM4000783

R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136

R-NT2RM4001178//tk08e03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA sequence.//0.77//96//62//AI457506

R-NT2RM4002420//w158b04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA sequence.//2.4e-85//438//94//AI857508

R-NT2RP2000198//nx19b11.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA sequence.//1.9e-45//270//91//AA738352

R-NT2RP2000551//tg80h11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA sequence.//3.3e-53//311//85//AI417680

R-NT2RP2000660//ns42a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA sequence.//4.3e-26//142//97//AA805691

R-NT2RP2001214//tw65g08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains element MSR1 repetitive element ;, mRNA seq

uence.//1.5e-57//289//97//AI680174

R-NT2RP2001460

R-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDN
A clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEI
N ZFP-1 ;, mRNA sequence.//6.0e-13//85//96//AA427992

R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:130846 3', mRNA sequence.//0.0016//208//65//R22302

R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.
4e-26//339//71//AB011096

R-NT2RP2002755//qd50d10.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA
clone IMAGE:1732915 3', mRNA sequence.//1.5e-26//419//66//AI190698

R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
IMAGE:2373639 3' similar to contains L1.t1 L1 repetitive element ;, mRN
A sequence.//1.8e-45//463//74//AI749673

R-NT2RP2003101//ty24h05.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:22
80057 3', mRNA sequence.//7.5e-73//347//99//AI758824

R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0
.0026//247//65//AB018294

R-NT2RP2004095//zv08c02.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAG
E:753026 3' similar to contains element MER32 repetitive element ;, mRNA
sequence.//9.6e-07//188//66//AA436455

R-NT2RP2004732//tu60a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2
255412 3' similar to contains Alu repetitive element;contains element L1
repetitive element ;, mRNA sequence.//4.3e-25//414//68//AI678956

R-NT2RP2004920//wd13h02.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:23
28051 3', mRNA sequence.//6.8e-91//483//93//AI694022

R-NT2RP2005454//yy77g09.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapien
s cDNA clone IMAGE:279616 3', mRNA sequence.//0.0070//325//59//N48302

R-NT2RP2005776//qq97d06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDN

A clone IMAGE:1939307 3', mRNA sequence.//7.5e-08//89//82//AI338419
R-NT2RP2005806//wc29h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:
2316625 3' similar to contains MER2.b3 MER2 repetitive element ;, mRNA s
equence.//3.2e-16//235//71//AI671398
R-NT2RP2005882//wo31f09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2
456969 3', mRNA sequence.//0.00095//352//59//AI925528
R-NT2RP3001282//wg35b03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA
clone IMAGE:2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199
R-NT2RP3001723//wo48e06.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2
458594 3', mRNA sequence.//4.2e-98//471//98//AI926617
R-NT2RP3002099//DKFZp564L227_s1 564 (synonym: hfbr2) Homo sapiens cDNA c
lone DKFZp564L227 3', mRNA sequence.//9.2e-50//329//87//AL037910
R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapi
ens cDNA clone IMAGE:595668 3', mRNA sequence.//1.4e-30//159//99//AA1731
72
R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR
.//0.43//66//75//AF035594
R-OVARC1000008//wa69e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone I
MAGE:2301454 3', mRNA sequence.//1.0e-77//376//98//AI699393
R-OVARC1000724//tf94b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2
106907 3', mRNA sequence.//0.71//27//100//AI380236
R-OVARC1000751//og93d04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1
455847 3', mRNA sequence.//3.5e-13//274//63//AA863306
R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clo
ne IMAGE:290906 5' similar to contains Alu repetitive element;contains e
lement PTR5 repetitive element ;, mRNA sequence.//3.5e-13//175//74//N994
64
R-PLACE1000814//tg49a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone I
MAGE:2112086 3' similar to contains L1.t2 L1 L1 repetitive element ;, mR

NA sequence.//2.2e-18//285//69//AI424789

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//4.0e-34//225//90//AF032387

R-PLACE1005549//tm26b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA sequence.//0.91//127//66//AI480253

R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5' similar to contains Alu repetitive element; contains LTR4 repetitive element ;, mRNA sequence.//2.4e-36//245//87//R92256

【 0 8 3 5 】

相同性検索結果データ 1 2.

全長塩基配列および推定アミノ酸配列に対する相同性検索結果データ

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//6.4E-99//457aa//45%//Q09996

C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344

C-HEMBA1000129//HYPOTHETICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//Q09884

C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738

C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%//Q61221

C-HEMBA1000231

C-HEMBA1000264

C-HEMBA1000280

C-HEMBA1000282

C-HEMBA1000303// "Mus musculus Plenty of SH3s (POSH) mRNA, complete cds."//7.1E-254//1440bp//87%//AF030131

C-HEMBA1000333//”Homo sapiens mRNA for KIAA0874 protein, partial cds.”//
4.8E-253//1148bp//99%//AB020681

C-HEMBA1000351

C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp56
6C243).//3.3E-287//815bp//98%//AL050274

C-HEMBA1000396

C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357

C-HEMBA1000442

C-HEMBA1000456

C-HEMBA1000504

C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490

C-HEMBA1000519

C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01
755

C-HEMBA1000542//”Rattus norvegicus mRNA for dipeptidyl peptidase III, co
mplete cds.”//2.2E-194//663bp//83%//D89340

C-HEMBA1000545

C-HEMBA1000557

C-HEMBA1000592//”Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.
”//0//1465bp//99%//AF121856

C-HEMBA1000594

C-HEMBA1000604

C-HEMBA1000622

C-HEMBA1000637

C-HEMBA1000655

C-HEMBA1000657//”Rattus norvegicus ADP-ribosylation factor-directed GTPa
se activating protein mRNA, complete cds.”//7.2E-156//1366bp//76%//U3577

6

C-HEMBA1000749

C-HEMBA1000769
C-HEMBA1000773
C-HEMBA1000774
C-HEMBA1000822
C-HEMBA1000843
C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//11
9aa//87%//P51689
C-HEMBA1000870
C-HEMBA1000908
C-HEMBA1000934
C-HEMBA1000972
C-HEMBA1000986
C-HEMBA1000991
C-HEMBA1001008
C-HEMBA1001059//”Human N-acetylgalactosamine 6-sulphatase (GALNS) gene,
exon 14.”//4.8E-169//786bp//99%//U06088
C-HEMBA1001094
C-HEMBA1001302//”Homo sapiens calcium binding protein precursor, mRNA, c
omplete cds.”//9.6E-258//682bp//94%//AF153686
C-HEMBA1001330
C-HEMBA1001497
C-HEMBA1001569//SYNAPTOSOMAL MEMBRANE PROTEIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2)
(VAMP-2).//2.3E-53//110aa//100%//P19065
C-HEMBA1001570
C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1
.6E-166//506aa//60%//P42803
C-HEMBA1001640
C-HEMBA1001655
C-HEMBA1001672//”Homo sapiens methyl-CpG binding domain-containing prote

in MBD3 (MBD3) mRNA, complete cds."//0//1707bp//98%//AF072247
 C-HEMBA1001711
 C-HEMBA1001723// "Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//4.7E-172//1240bp//81%//AF051155
 C-HEMBA1001746// "Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//7.6E-59//998bp//64%//AF098066
 C-HEMBA1001781
 C-HEMBA1001804// "Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//1637bp//99%//AF125158
 C-HEMBA1001822// "Mus musculus Ese2L protein mRNA, complete cds."//1.9E-235//1329bp//89%//AF132479
 C-HEMBA1001824
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.7E-51//234aa//41%//Q09332
 C-HEMBA1001910
 C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535
 C-HEMBA1001921// "Homo sapiens germinal center kinase related protein kinase mRNA, complete cds."//0//1850bp//99%//AF000145
 C-HEMBA1001939
 C-HEMBA1001950// "Homo sapiens mRNA for KIAA0971 protein, complete cds."//0//1974bp//99%//AB023188
 C-HEMBA1001967// "Homo sapiens NY-REN-57 antigen mRNA, partial cds."//0//1721bp//99%//AF155114
 C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%//AL050089
 C-HEMBA1002092// "Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds."//1.3E-271//1583bp//88%//U92703
 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357
 C-HEMBA1002150

C-HEMBA1002151//”Rattus norvegicus p34 mRNA, complete cds.”//1.1E-153//1059bp//82%//AF178669

C-HEMBA1002189

C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226

C-HEMBA1002229

C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087

C-HEMBA1002341//”Homo sapiens mRNA for KIAA0771 protein, partial cds.”//0//1514bp//99%//AB018314

C-HEMBA1002417//”Homo sapiens chromosome 19, cosmid R28784, complete sequence.”//1.4E-299//294bp//100%//AC005954

C-HEMBA1002547//”Homo sapiens agrin precursor mRNA, partial cds.”//0//1605bp//97%//AF016903

C-HEMBA1002703

C-HEMBA1002779

C-HEMBA1002816

C-HEMBA1002970

C-HEMBA1002999//”Rattus norvegicus lamina associated polypeptide 1C (LAP 1C) mRNA, complete cds.”//1.4E-171//1552bp//75%//U20286

C-HEMBA1003021

C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%//P24014

C-HEMBA1003079

C-HEMBA1003273

C-HEMBA1003304

C-HEMBA1003309

C-HEMBA1003376

C-HEMBA1003384

C-HEMBA1003531

C-HEMBA1003548
C-HEMBA1003556
C-HEMBA1003571
C-HEMBA1003579
C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//
32%//Q13105
C-HEMBA1003692
C-HEMBA1003720
C-HEMBA1003725
C-HEMBA1003729
C-HEMBA1003758
C-HEMBA1003773//”Mus musculus signal recognition particle receptor beta
subunit mRNA, complete cds.”//5.8E-81//511bp//86%//U17343
C-HEMBA1003783//”Mus musculus bromodomain-containing protein BP75 mRNA,
complete cds.”//1.1E-190//1204bp//84%//AF084259
C-HEMBA1003799
C-HEMBA1003804
C-HEMBA1003805//”Mus musculus KH domain RNA binding protein QKI-5A mRNA,
complete cds.”//0//988bp//95%//AF090402
C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40
484
C-HEMBA1003856
C-HEMBA1003866//”Mus musculus semaphorin VIa mRNA, complete cds.”//1.2E-
105//1192bp//70%//AF030430
C-HEMBA1003879
C-HEMBA1003880
C-HEMBA1003893
C-HEMBA1003908
C-HEMBA1003937

C-HEMBA1003942
C-HEMBA1003958
C-HEMBA1003976
C-HEMBA1003978//”Homo sapiens mRNA for KIAA0840 protein, partial cds.”//
0//1530bp//100%//AB020647
C-HEMBA1003985
C-HEMBA1004011
C-HEMBA1004024
C-HEMBA1004038
C-HEMBA1004045
C-HEMBA1004048
C-HEMBA1004111//”Homo sapiens mRNA for KIAA1276 protein, partial cds.”//
1.00E-163//751bp//99%//AB033102
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q141
41
C-HEMBA1004138
C-HEMBA1004143
C-HEMBA1004150
C-HEMBA1004168//”Homo sapiens geminin mRNA, complete cds.”//3.9E-208//95
1bp//99%//AF067855
C-HEMBA1004200
C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%//P51153
C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%//P40991
C-HEMBA1004238
C-HEMBA1004248//”Homo sapiens insulin induced protein 2 mRNA, complete c
ds.”//8.20E-175//552bp//97%//AF125392
C-HEMBA1004272
C-HEMBA1004274
C-HEMBA1004275//”Homo sapiens mRNA for KIAA1111 protein, partial cds.”//

0//1341bp//99%//AB029034

C-HEMBA1004286//”Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.”//0//1982bp//99%//AF022795

C-HEMBA1004312

C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%
//Q99676

C-HEMBA1004323

C-HEMBA1004327

C-HEMBA1004330

C-HEMBA1004341

C-HEMBA1004366

C-HEMBA1004372

C-HEMBA1004389//”Homo sapiens zinc finger DNA binding protein 99 (ZNF281)
) mRNA, complete cds.”//0//1437bp//99%//AF125158

C-HEMBA1004394

C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPI
ASE) (ROTAMASE) (CYCLOPHILIN-10).//3.2E-32//148aa//52%//P52017

C-HEMBA1004429

C-HEMBA1004460

C-HEMBA1004461

C-HEMBA1004502

C-HEMBA1004554

C-HEMBA1004560

C-HEMBA1004610

C-HEMBA1004629

C-HEMBA1004632

C-HEMBA1004637

C-HEMBA1004670

C-HEMBA1004672

C-HEMBA1004697
C-HEMBA1004711
C-HEMBA1004725
C-HEMBA1004730
C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743
C-HEMBA1004751
C-HEMBA1004752
C-HEMBA1004889// "Human C3f mRNA, complete cds."//6.70E-24//341aa//26%//U72515
C-HEMBA1004934
C-HEMBA1004944
C-HEMBA1004973
C-HEMBA1004977
C-HEMBA1005009// "Homo sapiens BAF53a (BAF53a) mRNA, complete cds."//0//1813bp//99%//AF041474
C-HEMBA1005083
C-HEMBA1005113
C-HEMBA1005133
C-HEMBA1005185
C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%//P39929
C-HEMBA1005252// "Homo sapiens mRNA for KIAA0585 protein, partial cds."//1.2E-268//1215bp//99%//AB011157
C-HEMBA1005296
C-HEMBA1005314
C-HEMBA1005331
C-HEMBA1005394
C-HEMBA1005403

C-HEMBA1005423//”Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)
mRNA, complete cds.”//2E-213//537bp//99%//AF041248

C-HEMBA1005468

C-HEMBA1005469

C-HEMBA1005474

C-HEMBA1005517

C-HEMBA1005518

C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//
Q60809

C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929

C-HEMBA1005576//”Homo sapiens mRNA for KIAA0463 protein, partial cds.”//
1.1E-181//835bp//99%//AB007932

C-HEMBA1005582//”TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYT
OSKELETAL TROPOMYOSIN).”//0.00000009//213aa//27%//P09492

C-HEMBA1005583

C-HEMBA1005595//”DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).”//2.3E-54//562aa/
/29%//P34036

C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp56
4K133).//2.2e-315//1448bp//99%//AL050012

C-HEMBA1005621//”Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds.”
//2.9E-224//1031bp//99%//AF139365

C-HEMBA1005666

C-HEMBA1005680

C-HEMBA1005685

C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY
SUBUNIT).//4.4E-17//167aa//34%//P25296

C-HEMBA1005746

C-HEMBA1005755

C-HEMBA1005813

C-HEMBA1005822
C-HEMBA1005834
C-HEMBA1005884
C-HEMBA1005891
C-HEMBA1005909
C-HEMBA1005911
C-HEMBA1005931
C-HEMBA1005963
C-HEMBA1005991
C-HEMBA1006005
C-HEMBA1006031//”Homo sapiens mRNA for putative phospholipase, complete
cds.”//0//1413bp//99%//AB019435
C-HEMBA1006067
C-HEMBA1006081
C-HEMBA1006091
C-HEMBA1006100
C-HEMBA1006108//”Homo sapiens mRNA for KIAA0943 protein, partial cds.”//
4.8E-245//764bp//99%//AB023160
C-HEMBA1006121
C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794
C-HEMBA1006155
C-HEMBA1006158//”Homo sapiens transcription factor forkhead-like 7 (FKHL
7) gene, complete cds.”//0//1551bp//99%//AF048693
C-HEMBA1006182
C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39
%//P05142
C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%/
/AF070557
C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//

0.00000002//62aa//53%/P42698

C-HEMBA1006259

C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-)//1.3E-123//20
0aa//73%/P10265

C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A
DENYLYLTRANSFERASE)//1E-210//490aa//77%/P25500

C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2//0.0000
00012//176aa//30%/P32505

C-HEMBA1006284

C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-)//4.2E-12//21
5aa//23%/P70473

C-HEMBA1006293

C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REG
ION//1.4E-48//248aa//43%/P38821

C-HEMBA1006349

C-HEMBA1006364

C-HEMBA1006381

C-HEMBA1006398// "Human L1 element L1.6 putative p150 gene, complete cds.
"//2E-277//1729bp//85%/U93563

C-HEMBA1006445// "Homo sapiens putative tumor supressor NOEY2 mRNA, compl
ete cds."//1.4E-270//1224bp//100%/U96750

C-HEMBA1006483

C-HEMBA1006492

C-HEMBA1006497

C-HEMBA1006502

C-HEMBA1006507// "Homo sapiens mRNA for KIAA0666 protein, partial cds."//
0//2334bp//99%/AB014566

C-HEMBA1006535

C-HEMBA1006559// "Mus musculus PRAJA1 (Praj1) mRNA, complete cds."//2.8E

-206//1107bp//83%//U06944

C-HEMBA1006566

C-HEMBA1006579

C-HEMBA1006583

C-HEMBA1006612

C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.000

00069//109aa//38%//Q58323

C-HEMBA1006643

C-HEMBA1006674

C-HEMBA1006682

C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
IN PMC1-TFG2 INTERGENIC REGION.//3.3E-22//241aa//31%//P53196

C-HEMBA1006717

C-HEMBA1006744

C-HEMBA1006754

C-HEMBA1006767

C-HEMBA1006789

C-HEMBA1006832

C-HEMBA1006885//"*Homo sapiens* gene for Proline synthetase associated, co
mplete cds."//0//1467bp//96%//AB018566

C-HEMBA1006900

C-HEMBA1006926

C-HEMBA1006941//*Homo sapiens* mRNA for putative thioredoxin-like protein.
//1.8E-226//1039bp//99%//AJ010841

C-HEMBA1006973//"*Homo sapiens* rab3-GAP regulatory domain mRNA, complete
cds."//5.6E-143//740bp//94%//AF004828

C-HEMBA1006993

C-HEMBA1007002

C-HEMBA1007062

C-HEMBA1007080

C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626

C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//99%//AL117450

C-HEMBA1007194// "Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds."//0//1588bp//99%//AF139658

C-HEMBA1007206

C-HEMBA1007256

C-HEMBA1007267

C-HEMBA1007281

C-HEMBA1007300// "Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds."//0//1519bp//99%//AF127479

C-HEMBA1007301

C-HEMBA1007319

C-HEMBA1007320

C-HEMBA1007327

C-HEMBA1007347

C-HEMBB1000005

C-HEMBB1000030

C-HEMBB1000048

C-HEMBB1000099

C-HEMBB1000141

C-HEMBB1000198

C-HEMBB1000217// "Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds."//0//1038bp//99%//AF090385

C-HEMBB1000218

C-HEMBB1000274

C-HEMBB1000312

C-HEMBB1000402
 C-HEMBB1000420
 C-HEMBB1000480
 C-HEMBB1000530
 C-HEMBB1000550
 C-HEMBB1000556//”Homo sapiens mRNA for KIAA0750 protein, complete cds.”/
 /6.3E-74//1213bp//64%//AB018293
 C-HEMBB1000586
 C-HEMBB1000592
 C-HEMBB1000593//”Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA,
 complete cds.”//1.3E-107//503bp//99%//AF067864
 C-HEMBB1000649
 C-HEMBB1000693//”Homo sapiens neuroanl mRNA, complete cds.”//0//2952bp//
 94%//AF040723
 C-HEMBB1000822
 C-HEMBB1000826
 C-HEMBB1000890
 C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-)./
 /1.10E-08//129aa//31%//P29122
 C-HEMBB1001008
 C-HEMBB1001020//”Homo sapiens mRNA for KIAA0889 protein, complete cds.”/
 /0//1812bp//98%//AB020696
 C-HEMBB1001051
 C-HEMBB1001112//”Homo sapiens sec61 homolog mRNA, complete cds.”//6E-145
 //961bp//83%//AF077032
 C-HEMBB1001221
 C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//5
 4%//P46938
 C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./

/7E-43//394aa//34%/P16157

C-HEMBB1001302

C-HEMBB1001335

C-HEMBB1001337

C-HEMBB1001356

C-HEMBB1001364

C-HEMBB1001366

C-HEMBB1001367

C-HEMBB1001527

C-HEMBB1001537

C-HEMBB1002359

C-HEMBB1002415

C-HEMBB1002457

C-HEMBB1002492

C-HEMBB1002495

C-HEMBB1002502

C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%/P27544

C-HEMBB1002600// "Homo sapiens tetraspan NET-5 mRNA, complete cds."//0//1
417bp//99%/AF089749

C-HEMBB1002607// "Homo sapiens vitamin D3 receptor interacting protein (D
RIP80) mRNA, complete cds."//2E-136//660bp//98%/AF105421

C-HEMBB1002684

C-HEMBB1002692

C-HEMBB1002697

C-HEMBB1002705// "Homo sapiens CGI-27 protein mRNA, complete cds."//7.80E
-285//841bp//96%/AF132961

C-MAMMA1000019

C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM
05).//8.2E-198//868bp//99%/Z47553

C-MAMMA1000025
C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//3
23aa//48%//P47226
C-MAMMA1000069
C-MAMMA1000084
C-MAMMA1000139
C-MAMMA1000163
C-MAMMA1000171
C-MAMMA1000173//”Homo sapiens src homology 3 domain-containing protein H
IP-55 mRNA, complete cds.”//2.6E-164//1044bp//87%//AF197060
C-MAMMA1000277
C-MAMMA1000278
C-MAMMA1000284//P.walti mRNA for rnp associated protein 55.//2.2E-109//8
64bp//76%//X99836
C-MAMMA1000309
C-MAMMA1000312
C-MAMMA1000313
C-MAMMA1000361
C-MAMMA1000388//”Homo sapiens UKLF mRNA for ubiquitous Kruppel like fact
or, complete cds.”//0//1466bp//99%//AB015132
C-MAMMA1000395
C-MAMMA1000410
C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./
/2.00E-30//119aa//53%//Q09232
C-MAMMA1000421
C-MAMMA1000422
C-MAMMA1000468
C-MAMMA1000472
C-MAMMA1000490

C-MAMMA1000524
 C-MAMMA1000567
 C-MAMMA1000612//”Rattus norvegicus G beta-like protein GBL mRNA, complete cds.”//1E-95//1115bp//72%//AF051155
 C-MAMMA1000623
 C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%//P48365
 C-MAMMA1000664
 C-MAMMA1000670
 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//4.4E-33//250aa//33%//P42660
 C-MAMMA1000713//L-RIBULOSE KINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524
 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1E-77//395aa//45%//O14646
 C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779
 C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9E-299//1033aa//55%//P87115
 C-MAMMA1000746
 C-MAMMA1000775
 C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%//P53500
 C-MAMMA1000831
 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.8E-40//101aa//54%//O27540
 C-MAMMA1000842
 C-MAMMA1000843
 C-MAMMA1000856
 C-MAMMA1000865
 C-MAMMA1000875

C-MAMMA1000906

C-MAMMA1000908

C-MAMMA1000914

C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//
AJ250711

C-MAMMA1000968

C-MAMMA1000979

C-MAMMA1001008//”Homo sapiens aspartic-like protease mRNA, complete cds.
”//2.50E-276//1263bp//99%//AF117892

C-MAMMA1001021

C-MAMMA1001041//”SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BET
A CHAIN) (FODRIN BETA CHAIN) (SPTBN1).”//1.6E-16//113aa//41%//Q01082

C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99
%//AJ237946

C-MAMMA1001075//”Homo sapiens CGI-72 protein mRNA, complete cds.”//1.3E-
181//397bp//98%//AF151830

C-MAMMA1001078

C-MAMMA1001091

C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%//P
51521

C-MAMMA1001110

C-MAMMA1001126

C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273

C-MAMMA1001143

C-MAMMA1001154

C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q9
2338

C-MAMMA1001215

C-MAMMA1001244

C-MAMMA1001259// "Mus musculus F-box protein FBX18 mRNA, partial cds."//2
.3E-271//1414bp//89%//AF184275

C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III./
/2.1E-52//630aa//30%//P34537

C-MAMMA1001343

C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp5
6400823).//0//2131bp//99%//AL080121

C-MAMMA1001419

C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE)
(FRAGMENT).//6.5E-129//260aa//92%//P52623

C-MAMMA1001510

C-MAMMA1001522

C-MAMMA1001576// "Human gamma-tubulin mRNA, complete cds."//7.5E-276//156
1bp//90%//M61764

C-MAMMA1001604

C-MAMMA1001620

C-MAMMA1001635

C-MAMMA1001649

C-MAMMA1001686

C-MAMMA1001692

C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8
.5E-32//171aa//36%//P21573

C-MAMMA1001754// "Homo sapiens CGI-11 protein mRNA, complete cds."//0//18
37bp//98%//AF132945

C-MAMMA1001757

C-MAMMA1001764

C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45/
/351aa//38%//Q58556

C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79

%//X85991
 C-MAMMA1001790
 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%/Q
 07230
 C-MAMMA1001858
 C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%/P22793
 C-MAMMA1001970
 C-MAMMA1002042
 C-MAMMA1002068
 C-MAMMA1002153
 C-MAMMA1002156
 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//
 157aa//70%/P15880
 C-MAMMA1002174
 C-MAMMA1002209
 C-MAMMA1002219//”Homo sapiens mRNA for KIAA1067 protein, partial cds.”//
 1.1E-181//861bp//98%/AB028990
 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-
 2B GDP-GTP EXCHANGE FACTOR).//8.8E-217//310aa//86%/P70541
 C-MAMMA1002243
 C-MAMMA1002268//”Mus musculus sphingosine kinase (SPHK1a) mRNA, partial
 cds.”//1E-190//1624bp//76%/AF068748
 C-MAMMA1002269
 C-MAMMA1002292
 C-MAMMA1002294
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1
 .1E-214//881bp//97%/AJ011679
 C-MAMMA1002312
 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%/

/X85991

C-MAMMA1002333

C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%/P
40882

C-MAMMA1002353

C-MAMMA1002355

C-MAMMA1002356

C-MAMMA1002362

C-MAMMA1002380

C-MAMMA1002384

C-MAMMA1002427

C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).
//1E-11//128aa//36%/P47623

C-MAMMA1002485// "Homo sapiens stanniocalcin-related protein mRNA, comple
te cds."//0//1822bp//99%/AF098462

C-MAMMA1002494

C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC RE
GION.//1.2E-34//337aa//31%/P43571

C-MAMMA1002530// "Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 ga
mma) mRNA, complete cds."//0//1910bp//99%/AF065214

C-MAMMA1002554

C-MAMMA1002585// "Homo sapiens mRNA for KIAA0860 protein, complete cds."/
/0//1405bp//99%/AB020667

C-MAMMA1002598

C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//9.5E-16//159aa//37%/Q09931

C-MAMMA1002655// "Homo sapiens mRNA for ganglioside sialidase, complete c
ds."//0//1515bp//99%/AB008185

C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA
LIGASE) (ACYL- ACTIVATING ENZYME).//1.1E-45//618aa//26%/P27550

C-MAMMA1002673

C-MAMMA1002684//”Homo sapiens mRNA for KIAA0214 protein, complete cds.”/
/0//3174bp//99%/D86987

C-MAMMA1002711

C-MAMMA1002769//”Homo sapiens cell cycle progression restoration 8 prote
in (CPR8) mRNA, complete cds.”//2.2E-25//330bp//77%/AF011794

C-MAMMA1002775

C-MAMMA1002782

C-MAMMA1002796

C-MAMMA1002807

C-MAMMA1002838

C-MAMMA1002842//”Mus musculus c-Cbl associated protein CAP mRNA, complet
e cds.”//2.6E-58//373bp//81%/U58883

C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTE
IN).//1.4E-160//305aa//85%/P48059

C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5
.7E-30//214aa//35%/P48060

C-MAMMA1002886

C-MAMMA1002890

C-MAMMA1002938//”Homo sapiens mRNA for KIAA0698 protein, complete cds.”/
/8.4E-252//1139bp//100%/AB014598

C-MAMMA1002964

C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.7E-123//370aa//66%/Q02874

C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.4E-46//332aa//36%//
P06746

C-MAMMA1003015

C-MAMMA1003019

C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2
.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.9E-13//108aa//
33%/P23851

C-MAMMA1003039

C-MAMMA1003044

C-MAMMA1003049

C-MAMMA1003056

C-MAMMA1003057//MD6 PROTEIN.//3.1E-225//419aa//97%/Q60584

C-MAMMA1003066

C-MAMMA1003099

C-MAMMA1003104

C-MAMMA1003113//”Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, com
plete cds.”//1.1E-234//1178bp//86%/AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.2E-105//217aa//89%/P4673
5

C-MAMMA1003135

C-MAMMA1003146//Homo sapiens mRNA for GALT3 protein.//4.3E-218//996bp//9
9%/Y15062

C-MAMMA1003150//”Homo sapiens mRNA for KIAA1096 protein, partial cds.”//
0//1342bp//99%/AB029019

C-MAMMA1003166//”Homo sapiens MLL septin-like fusion protein (MSF) mRNA,
complete cds.”//3.10E-158//592bp//97%/AF123052

C-NT2RM1000032

C-NT2RM1000035//”Human mRNA for KIAA0199 gene, partial cds.”//0//2948bp/
/99%/D83782

C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REG
ION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%/P37596

C-NT2RM1000055//”Homo sapiens mRNA for KIAA0829 protein, partial cds.”//
0//3111bp//99%/AB020636

C-NT2RM1000059

C-NT2RM1000062

C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%/P87072

C-NT2RM1000119

C-NT2RM1000127

C-NT2RM1000131//”Homo sapiens mRNA for KIAA0792 protein, complete cds.”//0//2980bp//99%/AB018335

C-NT2RM1000132//”Homo sapiens NADH:ubiquinone oxidoreductase NDUF5 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.”//7.8E-110//516bp//99%/AF044959

C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-38//469aa//27%/P49902

C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%/P87072

C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.1E-10//94aa//47%/042643

C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%/AJ245820

C-NT2RM1000244//”Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.”//2E-126//592bp//99%/U81002

C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%/X73882

C-NT2RM1000256//”Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.”//0//3012bp//99%/AB016789

C-NT2RM1000260//”Human mRNA for KIAA0130 gene, complete cds.”//0//3139bp//98%/D50920

C-NT2RM1000271

C-NT2RM1000300

C-NT2RM1000314//”Human mRNA for KIAA0159 gene, complete cds.”//0//4349bp

//99%//D63880

C-NT2RM1000354// "Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds."//7.4E-245//2101bp//68%//AF111423

C-NT2RM1000355// "Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds."//0//1599bp//99%//AF152462

C-NT2RM1000365

C-NT2RM1000377// "Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds."//3.2E-196//1016bp//94%//AF179212

C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000019//67aa//31%//P53915

C-NT2RM1000399

C-NT2RM1000430// "Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."//1.4E-185//1486bp//81%//AF084928

C-NT2RM1000555// "Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%//AB020692

C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372

C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636

C-NT2RM1000661// "Homo sapiens translation initiation factor 4e mRNA, complete cds."//4.3E-210//960bp//99%//AF038957

C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989

C-NT2RM1000672

C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440

C-NT2RM1000699

C-NT2RM1000741// "Homo sapiens mRNA for KIAA0567 protein, partial cds."//1.1E-295//1338bp//99%//AB011139

C-NT2RM1000742// "Homo sapiens AC133 antigen mRNA, complete cds."//0//352

4bp//99%//AF027208

C-NT2RM1000746//”Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.”//6.70E-227//1043bp//99%//AF141310

C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202

C-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808

C-NT2RM1000780

C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//1.1E-98//571bp//89%//Z97207

C-NT2RM1000802

C-NT2RM1000811//”Homo sapiens AC133 antigen mRNA, complete cds.”//0//3524bp//99%//AF027208

C-NT2RM1000826//”Homo sapiens mRNA for KIAA0885 protein, complete cds.”//0//2885bp//99%//AB020692

C-NT2RM1000829

C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%//P16157

C-NT2RM1000852//”Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.”//0//2206bp//99%//AF077033

C-NT2RM1000857//”Homo sapiens mRNA for KIAA0962 protein, partial cds.”//0//3716bp//99%//AB023179

C-NT2RM1000874//”Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.”//1.4E-244//1113bp//99%//AF043733

C-NT2RM1000882//”Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.”//4.30E-122//1394bp//69%//AF126799

C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa//30%//P34537

C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700

C-NT2RM1000898//”ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).”//8.9E-26//22
9aa//29%//P02583

C-NT2RM1000905//”Homo sapiens HSPC021 mRNA, complete cds.”//0//1480bp//9
9%//AF077207

C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.
//1E-15//266aa//26%//P46577

C-NT2RM1000927

C-NT2RM1000962

C-NT2RM1000978

C-NT2RM1001003//”Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA,
complete cds.”//0//2230bp//99%//AF030233

C-NT2RM1001043

C-NT2RM1001066

C-NT2RM1001072//”1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERA
SE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II
) (PLC-148).”//8.3E-47//259aa//35%//P08487

C-NT2RM1001085//”Rattus norvegicus brain specific cortactin-binding prot
ein CBP90 mRNA, partial cds.”//3.7E-32//460bp//64%//AF053768

C-NT2RM1001102//”Human HEM45 mRNA, complete cds.”//2.3E-27//482bp//63%//
U88964

C-NT2RM1001105

C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp5
64F0522).//0//1756bp//99%//AL049943

C-NT2RM2000420

C-NT2RM2000566//”Homo sapiens integrin alpha-7 mRNA, complete cds.”//0//
2519bp//96%//AF032108

C-NT2RM2000609

C-NT2RM2000612//”Rattus norvegicus ADP-ribosylation factor-directed GTPa
se activating protein mRNA, complete cds.”//2.6E-106//1069bp//74%//U3577

6

C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-103//2
49aa//73%//P28160

C-NT2RM2001588

C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ
132440

C-NT2RM2001613//”Homo sapiens sec61 homolog mRNA, complete cds.”//0//260
1bp//99%//AF084458

C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%//P35844

C-NT2RM2001648//”Homo sapiens sec61 homolog mRNA, complete cds.”//0//242
1bp//99%//AF084458

C-NT2RM2001652//”Homo sapiens guanine nucleotide exchange factor mRNA, c
omplete cds.”//0//2608bp//99%//AF111162

C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.4E-39//161aa//34%//P
20107

C-NT2RM2001664//”Homo sapiens IkappaB kinase complex associated protein
(IKAP) mRNA, complete cds.”//0//2471bp//99%//AF044195

C-NT2RM2001668//”Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alter
native splice product ending in intron 11, complete cds.”//6.2E-16//464b
p//62%//AF083391

C-NT2RM2001671//”Oryctolagus cuniculus sarcolemmal associated protein (S
LAP1) mRNA, complete cds.”//0//1843bp//94%//U21155

C-NT2RM2001675

C-NT2RM2001681

C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//
4.60E-20//253aa//30%//Q09674

C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA.//0//2016bp//99%//AF
103804

C-NT2RM2001696

C-NT2RM2001698//”Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.”//6.2E-253//1170bp//99%//AB028600

C-NT2RM2001700//”ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).”//5.7E-130//536aa//49%//P50544

C-NT2RM2001716

C-NT2RM2001723

C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).”//7.2E-16//381aa//27%//Q09931

C-NT2RM2001743//”Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.”//0//1498bp//99%//AF011792

C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.”//8.8E-11//119aa//36%//Q92609

C-NT2RM2001760//”Homo sapiens sec61 homolog mRNA, complete cds.”//0//2379bp//99%//AF084458

C-NT2RM2001768

C-NT2RM2001771//ZINC FINGER PROTEIN 135.”//6.4E-154//394aa//64%//P52742

C-NT2RM2001782//”Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.”//0//1470bp//99%//AF135422

C-NT2RM2001784

C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).”//0//2146bp//99%//AL050118

C-NT2RM2001813

C-NT2RM2001823//CHD1 PROTEIN.”//1.8E-106//631aa//39%//P32657

C-NT2RM2001839//”Homo sapiens calumein (Calu) mRNA, complete cds.”//0//2415bp//97%//AF013759

C-NT2RM2001840

C-NT2RM2001855

C-NT2RM2001867//”Homo sapiens mRNA for KIAA0943 protein, partial cds.”//

0//967bp//99%//AB023160

C-NT2RM2001879

C-NT2RM2001983//”Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.”//0//1658bp//98%//AF089816

C-NT2RM2002145//”Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.”//8.5E-191//1524bp//81%//AF084928

C-NT2RM4000027

C-NT2RM4000030//LAS1 PROTEIN.//5.6E-12//184aa//32%//P36146

C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003

C-NT2RM4000155//”THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).”//1.2E-157//321aa//61%//P26639

C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.6E-21//785bp//60%//X67336

C-NT2RM4000167//”Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.”//0//1946bp//99%//AF071592

C-NT2RM4000199

C-NT2RM4000200

C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.9E-32//170aa//41%/Q16600

C-NT2RM4000233//”Mus musculus semaphorin VIa mRNA, complete cds.”//3.4E-231//1395bp//86%//AF030430

C-NT2RM4000244

C-NT2RM4000251

C-NT2RM4000265

C-NT2RM4000324

C-NT2RM4000327

C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292

C-NT2RM4000425

C-NT2RM4000433//”Mus musculus retinoic acid-responsive protein (Stra6) m

RNA, complete cds."//4.1E-271//2085bp//77%//AF062476
C-NT2RM4000514
C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.4E-89//389aa//43%//Q
07230
C-NT2RM4000532
C-NT2RM4000534
C-NT2RM4000603
C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//1
08aa//31%//Q00808
C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA
LIGASE) (ACYL- ACTIVATING ENZYME).//2.7E-146//420aa//60%//P27550
C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aa//30%//P7
4168
C-NT2RM4000689
C-NT2RM4000698
C-NT2RM4000700
C-NT2RM4000712// "Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA
, partial cds."//1E-136//1104bp//77%//AF022789
C-NT2RM4000717
C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa
//29%//P52154
C-NT2RM4000734// "Homo sapiens mRNA for KIAA0760 protein, partial cds."//
0//2273bp//99%//AB018303
C-NT2RM4000741// "Homo sapiens hSGT1 mRNA for hSgt1p, complete cds."//0//
2184bp//99%//D88208
C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53
%//Q99676
C-NT2RM4000764
C-NT2RM4000778

C-NT2RM4000787

C-NT2RM4000790

C-NT2RM4000795//”Homo sapiens mRNA for KIAA0951 protein, complete cds.”/
/0//1847bp//96%//AB023168

C-NT2RM4000796

C-NT2RM4000798//”Homo sapiens brefeldin A-inhibited guanine nucleotide-e
xchange protein 2 mRNA, complete cds.”//0//2603bp//99%//AF084521

C-NT2RM4000813

C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.3
4) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682

C-NT2RM4000833

C-NT2RM4000848

C-NT2RM4000852

C-NT2RM4000855

C-NT2RM4000887

C-NT2RM4000895

C-NT2RM4000950

C-NT2RM4000979

C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp5
86G0518).//0//2259bp//100%//AL050092

C-NT2RM4001032

C-NT2RM4001047//MO25 PROTEIN.//8E-140//333aa//80%//Q06138

C-NT2RM4001054//”Homo sapiens sec61 homolog mRNA, complete cds.”//3.1E-1
90//1315bp//81%//AF077032

C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.
//0.000000032//165aa//33%//Q09820

C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II./
/5.9E-86//292aa//48%//Q09417

C-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//1E-11//103aa//38%//Q01704

C-NT2RM4001151

C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.1E-197//445aa//78%//Q2
7969

C-NT2RM4001160

C-NT2RM4001187

C-NT2RM4001191// "Homo sapiens clone 24963 mRNA sequence, complete cds."//
/0//1950bp//99%//AF131737

C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135//375aa//60%//P52742

C-NT2RM4001203// "Homo sapiens mRNA for KIAA0839 protein, partial cds."//
0//3047bp//99%//AB020646

C-NT2RM4001204// "Homo sapiens mRNA for KIAA1089 protein, partial cds."//
0//2349bp//99%//AB029012

C-NT2RM4001217// "Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA,
complete cds."//7.3E-148//1409bp//72%//AF059611

C-NT2RM4001256// "Xenopus laevis putative Zic3 binding protein mRNA, comp
lete cds."//4.30E-55//289bp//77%//AF129131

C-NT2RM4001258

C-NT2RM4001309

C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137)
(PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676

C-NT2RM4001316// "ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR
(EC 1.3.99.3) (MCAD)."//2.3E-31//334aa//30%//P08503

C-NT2RM4001320// "Homo sapiens mRNA for Neuroblastoma, complete cds."//1.
8E-39//728bp//64%//D89016

C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171
aa//37%//P32626

C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC
REGION.//8.1E-30//265aa//33%//P53742

C-NT2RM4001347// "Homo sapiens NY-REN-25 antigen mRNA, partial cds."//0//

2300bp//99%//AF155103

C-NT2RM4001371//”Homo sapiens IDN3 mRNA, partial cds.”//0//2524bp//99%//
AB019494

C-NT2RM4001382//”Homo sapiens RanBP7/importin 7 mRNA, complete cds.”//2.

2E-237//1079bp//99%//AF098799

C-NT2RM4001384

C-NT2RM4001410

C-NT2RM4001411//”Mus musculus Pro-rich, PH, SH2 domain-containing signal
ing mediator (PSM) mRNA, complete cds.”//0//1962bp//87%//AF020526

C-NT2RM4001412//”Homo sapiens nGAP mRNA, complete cds.”//0//1918bp//99%/
/AF047711

C-NT2RM4001414

C-NT2RM4001437

C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA
LIGASE) (ILERS).//1.4E-118//444aa//46%//P73505

C-NT2RM4001454

C-NT2RM4001455

C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%//P52737

C-NT2RM4001489//”Homo sapiens mRNA for KIAA0685 protein, complete cds.”/
/0//1810bp//99%//AB014585

C-NT2RM4001522

C-NT2RM4001557//”Homo sapiens mRNA for KIAA1040 protein, partial cds.”//
0//1547bp//97%//AB028963

C-NT2RM4001565

C-NT2RM4001566//”Homo sapiens mRNA for KIAA1114 protein, complete cds.”/
/0//1900bp//99%//AB029037

C-NT2RM4001582//”Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, com
plete cds.”//1.5E-284//1082bp//90%//AF071317

C-NT2RM4001592//”Homo sapiens mRNA for KIAA1122 protein, partial cds.”//

0//2170bp//99%//AB032948

C-NT2RM4001594

C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750

C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203
aa//39%//Q12600

C-NT2RM4001629//”MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LAR
GE HOMOLOG 3).”//1.5E-93//278aa//38%//Q13368

C-NT2RM4001650

C-NT2RM4001662

C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REG
ION.//2.7E-84//410aa//42%//P37339

C-NT2RM4001682

C-NT2RM4001710

C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q141
41

C-NT2RM4001715

C-NT2RM4001731//”Homo sapiens mRNA for KIAA1004 protein, partial cds.”//
0//1922bp//100%//AB023221

C-NT2RM4001746

C-NT2RM4001754

C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-
).//4.1E-186//639aa//58%//Q05512

C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q
03164

C-NT2RM4001810//”Homo sapiens mRNA for KIAA0863 protein, complete cds.”/
/0//2377bp//99%//AB020670

C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346

C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-55//32
5aa//37%//P28160

C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%/P51523

C-NT2RM4001836

C-NT2RM4001841//”Homo sapiens mRNA for KIAA0920 protein, complete cds.”/0//1861bp//98%/AB023137

C-NT2RM4001842

C-NT2RM4001856

C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%/P79779

C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%/Y17711

C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//36%/Q15404

C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%/P47486

C-NT2RM4001922//”Homo sapiens mRNA for KIAA0957 protein, complete cds.”/0//2165bp//99%/AB023174

C-NT2RM4001930//”Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.”//0//1930bp//99%/AF102851

C-NT2RM4001940//”Homo sapiens timeless homolog mRNA, complete cds.”//0//2087bp//99%/AF098162

C-NT2RM4001953

C-NT2RM4001965

C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%/X99330

C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%/P51523

C-NT2RM4001984

C-NT2RM4001987//”NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSO

R (N-CAM 180) [CONTAINS: N-CAM 140].">//3.2E-17//281aa//30%/P16170
 C-NT2RM4002013//HYPOTHETICAL 89.4 KD. TRP-ASP REPEATS CONTAINING PROTEIN
 IN PMT6-PCT1 INTERGENIC REGION.//6.9E-94//589aa//35%/P42935
 C-NT2RM4002018
 C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.9E-53//1585bp/
 /60%/AF104260
 C-NT2RM4002044
 C-NT2RM4002054
 C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, com
 plete cds.//0//1865bp//99%/U82267
 C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protei
 n complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71%
 //AF117755
 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41
 %//Q04652
 C-NT2RM4002128
 C-NT2RM4002140
 C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%/P24014
 C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2
 671bp//99%/AF084535
 C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%/P21590
 C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-A
 LPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.2E-33//688aa
 //27%/P08640
 C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//
 /3E-37//122aa//72%/Q07803
 C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-
 1) mRNA, complete cds.//0//2452bp//100%/AF157028
 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%/

P40809

C-NT2RM4002251//”ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N- ACETYLGLUCO
SAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL- OLIGOSACCHARIDE-GLYCOPROT
EIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).”//2.2E-36/
/320aa//38%/P27808

C-NT2RM4002256

C-NT2RM4002266

C-NT2RM4002281

C-NT2RM4002287

C-NT2RM4002294

C-NT2RM4002301

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%/P48778

C-NT2RM4002339

C-NT2RM4002344

C-NT2RM4002373//”Homo sapiens mRNA for KIAA0649 protein, complete cds.”/
/0//2666bp//99%/AB014549

C-NT2RM4002374

C-NT2RM4002383

C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA
LIGASE) (ACYL- ACTIVATING ENZYME).//1.3E-29//275aa//30%/P27095

C-NT2RM4002438//”Xenopus laevis putative Zic3 binding protein mRNA, comp
lete cds.”//1.1E-49//611bp//70%/AF129131

C-NT2RM4002446

C-NT2RM4002452

C-NT2RM4002457

C-NT2RM4002460//”ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROT
EINS GP70, GP20].”//0.0000016//226aa//24%/P51515

C-NT2RM4002493

C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//3

66aa//27%//Q00808

C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%//P55137

C-NT2RM4002558//”Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.”//0//1797bp//99%//AF055899

C-NT2RM4002567

C-NT2RM4002593

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%//P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//2.3E-101//488aa//45%//032038

C-NT2RP1000324

C-NT2RP1000363//”Homo sapiens mRNA for KIAA0638 protein, partial cds.”//0//1345bp//99%//AB014538

C-NT2RP1000418

C-NT2RP1000513//”Human NifU-like protein (hNifU) mRNA, partial cds.”//6.50E-171//516bp//99%//U47101

C-NT2RP1000721

C-NT2RP1000730

C-NT2RP1000767

C-NT2RP1000836

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//33%//Q09531

C-NT2RP1000943

C-NT2RP1001033//”Homo sapiens delta-tubulin mRNA, complete cds.”//2.10E-285//1290bp//100%//AF201333

C-NT2RP1001073//”Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.”//8.1E-107//504bp//99%//AF182291

C-NT2RP1001199

C-NT2RP1001248

C-NT2RP1001253//”Homo sapiens oscillin (hLn) mRNA, complete cds.”//0//20

20bp//99%//AF029914
 C-NT2RP1001286
 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//3
 2%//Q12024
 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//3
 2%//Q12024
 C-NT2RP1001310//”Homo sapiens mitochondrial carrier homolog 1 isoform a
 mRNA, partial cds; nuclear gene for mitochondrial product.”//0//1732bp//
 99%//AF176006
 C-NT2RP1001361//”Homo sapiens NADH-ubiquinone oxidoreductase subunit B14
 .5B homolog mRNA, complete cds.”//6.5E-116//541bp//100%//AF070652
 C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC RE
 GION.//2.7E-22//284aa//25%//P40074
 C-NT2RP1001432
 C-NT2RP2000040//”Homo sapiens mRNA for KIAA0747 protein, partial cds.”//
 0//2648bp//99%//AB018290
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH
 2 gene).//7.9E-20//265bp//73%//AJ242730
 C-NT2RP2000098
 C-NT2RP2000108
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.7E-41//278aa/
 /36%//P40556
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE S
 UBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUB
 UNIT) (DNA-BINDING PROTEIN PO-GA).//7.1E-12//213aa//23%//P35251
 C-NT2RP2000289
 C-NT2RP2000327
 C-NT2RP2000337
 C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910

C-NT2RP2000459
C-NT2RP2000498
C-NT2RP2000758
C-NT2RP2001137
C-NT2RP2001149
C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%/P37370
C-NT2RP2001173// "Homo sapiens mRNA for KIAA0480 protein, complete cds."/
/0//1780bp//99%/AB007949
C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6E-1
0//88aa//38%/P18722
C-NT2RP2001196
C-NT2RP2001226
C-NT2RP2001268// "Homo sapiens mRNA for KIAA0810 protein, partial cds."//
0//3301bp//98%/AB018353
C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-AL
PHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT).//4.4E-91//179aa//99%/P2866
3
C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%/P
20107
C-NT2RP2001312
C-NT2RP2001327// "TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHE
LIAL (B12 PROTEIN)."//5.5E-116//311aa//71%/Q13829
C-NT2RP2001328
C-NT2RP2001366
C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//2
5%/Q02817
C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.2
1.-).//8.4E-192//581aa//54%/P93647
C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%/Y1

8004

C-NT2RP2001420//”Mus musculus nuclear protein NIP45 mRNA, complete cds.”
//9E-112//742bp//82%//U76759

C-NT2RP2001450

C-NT2RP2001467

C-NT2RP2001506

C-NT2RP2001511//”Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.”//3.2E-297//2206bp//75%//AF093097

C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL
AR1.//0//2502bp//99%//Y14494

C-NT2RP2001536//”Homo sapiens X-ray repair cross-complementing protein 3
(XRCC3) mRNA, complete cds.”//0//2326bp//99%//AF035586

C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992

C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//
8.2E-29//294aa//31%//Q09837

C-NT2RP2001581

C-NT2RP2001597//”RYANODINE RECEPTOR, CARDIAC MUSCLE.”//0.000000036//127a
a//36%//P30957

C-NT2RP2001628

C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-
PHOSPHO-D- GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%//P4
2897

C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS)
(FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1
) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//
97%//P14324

C-NT2RP2001813

C-NT2RP2001883//”Homo sapiens CGI-01 protein mRNA, complete cds.”//0//23
06bp//99%//AF132936

C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%//P53946
 C-NT2RP2001947
 C-NT2RP2001985//”Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.”//2.00E-38//435bp//67%//AF090989
 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%//Q08469
 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.7E-47//247aa//52%//P35331
 C-NT2RP2002058//”Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.”//0//2510bp//99%//AF083217
 C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.5E-294//1334bp//99%//AF052183
 C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%//P18490
 C-NT2RP2002079//”HISTONE H1, GONADAL.”//4.4E-11//214aa//34%//P02256
 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%//AJ007509
 C-NT2RP2002185//”Homo sapiens ubiquilin mRNA, complete cds.”//0//1789bp//99%//AF176069
 C-NT2RP2002193//”Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.”//0//2809bp//99%//AB021868
 C-NT2RP2002231
 C-NT2RP2002235
 C-NT2RP2002252//”Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.”//0//3118bp//91%//L38621
 C-NT2RP2002292
 C-NT2RP2002408
 C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%//P46037
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//6.50E-07//171a

a//27%/P30620

C-NT2RP2002498

C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%/Q02386

C-NT2RP2002520//”Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.”//3.70E-34//668bp//61%/AF105427

C-NT2RP2002549

C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%/P19076

C-NT2RP2002706

C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%/P55194

C-NT2RP2002800

C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%/P14922

C-NT2RP2002891

C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.1E-87//395aa//40%/Q18964

C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%/P52737

C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%/P70700

C-NT2RP2003034

C-NT2RP2003099

C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%/P13117

C-NT2RP2003157//”Homo sapiens CGI-74 protein mRNA, complete cds.”//0//2037bp//99%/AF151832

C-NT2RP2003158//”Homo sapiens mRNA for proteasome subunit p58, complete cds.”//0//2091bp//99%/D67025

C-NT2RP2003165

C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein whic

h interacts with transcription factor Spl.//0//1544bp//99%//AJ242978
 C-NT2RP2003277//”Homo sapiens mRNA for KIAA0625 protein, partial cds.”//
 0//3788bp//99%//AB014525
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4)
 (RNA-3' - PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%//Q23400
 C-NT2RP2003297
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%//Q07866
 C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%//P17886
 C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.
 000022//261aa//24%//P48754
 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//15
 09bp//99%//AJ133769
 C-NT2RP2003393
 C-NT2RP2003445
 C-NT2RP2003466//”Homo sapiens delta-6 fatty acid desaturase mRNA, comple
 te cds.”//0//2194bp//99%//AF126799
 C-NT2RP2003480//”Homo sapiens zinc finger DNA binding protein 99 (ZNF281
) mRNA, complete cds.”//0//3012bp//99%//AF125158
 C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4
 E-14//106aa//46%//P04175
 C-NT2RP2003511
 C-NT2RP2003513//”Human mRNA for KIAA0270 gene, partial cds.”//0//2137bp/
 /97%//D87460
 C-NT2RP2003567//”Homo sapiens mRNA for KIAA0462 protein, partial cds.”//
 0//2343bp//99%//AB007931
 C-NT2RP2003604//”Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA,
 complete cds.”//0//2442bp//99%//AF030233
 C-NT2RP2003691
 C-NT2RP2003713//”Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA,

complete cds."//0//2018bp//99%//AF073344
C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).
//0//869aa//80%//P53620
C-NT2RP2003764
C-NT2RP2003769
C-NT2RP2003777
C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3
.7E-21//137aa//43%//Q11076
C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION P
ROTEIN).//0.00000016//117aa//29%//Q91955
C-NT2RP2003981//"Homo sapiens mRNA for KIAA0804 protein, partial cds."//
0//3046bp//99%//AB018347
C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp56
4A026).//0//2514bp//99%//AL050367
C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599
C-NT2RP2004066//"Human DNA sequence from clone 134019 on chromosome 1p36
.11-36.33, complete sequence."//0//2410bp//99%//AL034555
C-NT2RP2004081
C-NT2RP2004124
C-NT2RP2004152
C-NT2RP2004165
C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION
FACTOR RU49).//5.6E-31//424aa//28%//Q07231
C-NT2RP2004239//"Homo sapiens lok mRNA for protein kinase, complete cds.
"//0//3044bp//99%//AB015718
C-NT2RP2004245
C-NT2RP2004364
C-NT2RP2004365
C-NT2RP2004366//"Homo sapiens mRNA for KIAA0986 protein, partial cds."//

0//2790bp//97%//AB023203

C-NT2RP2004373

C-NT2RP2004476//”Homo sapiens cyclin L ania-6a mRNA, complete cds.”//0//

2075bp//99%//AF180920

C-NT2RP2004551

C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//

625aa//40%//Q09903

C-NT2RP2004600

C-NT2RP2004664//”Homo sapiens mRNA for KIAA0460 protein, partial cds.”//

0//2368bp//99%//AB007929

C-NT2RP2004743

C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RIC

H KINASE 1).//1.3E-26//190aa//41%//P38692

C-NT2RP2004816//”Homo sapiens H beta 58 homolog mRNA, complete cds.”//0//

/2144bp//96%//AF054179

C-NT2RP2004861

C-NT2RP2004897

C-NT2RP2004933//”Homo sapiens mRNA for ZIP-kinase, complete cds.”//0//21

03bp//99%//AB007144

C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386

C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL AD

DITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFER

ASE).//4E-91//218aa//44%//Q92089

C-NT2RP2005162//”Homo sapiens aspartyl aminopeptidase mRNA, complete cds

.”//0//1615bp//99%//AF005050

C-NT2RP2005204//”Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA

1) mRNA, complete cds.”//0//1262bp//99%//AF090385

C-NT2RP2005227

C-NT2RP2005287

C-NT2RP2005288// "Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds."//0//2992bp//99%//AF060219

C-NT2RP2005490// "Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds."//1.8E-175//1102bp//83%//AF053628

C-NT2RP2005539// "Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//1560bp//99%//AB020657

C-NT2RP2005605// QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053

C-NT2RP2005722// "Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds."//0//2545bp//99%//AB011414

C-NT2RP2005732

C-NT2RP2005784// "Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds."//0//2191bp//92%//AF155120

C-NT2RP2005812// HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//318aa//31%//P40004

C-NT2RP2005859// "Homo sapiens mRNA for KIAA0863 protein, complete cds."//0//1649bp//99%//AB020670

C-NT2RP2006023

C-NT2RP2006334// Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//AL080155

C-NT2RP2006441

C-NT2RP3000002

C-NT2RP3000050// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//53%//Q05481

C-NT2RP3000055

C-NT2RP3000068

C-NT2RP3000080

C-NT2RP3000085// ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CO

NTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)] ./1.9E-123//436aa//50%/P46401

C-NT2RP3000092

C-NT2RP3000109//P54 PROTEIN PRECURSOR./0.0000065//358aa//22%/P13692

C-NT2RP3000134

C-NT2RP3000149

C-NT2RP3000197

C-NT2RP3000207//”GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).”//2.9E-11//721aa //23%/P08640

C-NT2RP3000233//”Human DNA sequence from clone 22D12 on chromosome Xq21. 1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins. Contains ESTs and GSSs, complete sequence.”//0//1462bp//99%/AL035424

C-NT2RP3000235

C-NT2RP3000247

C-NT2RP3000267

C-NT2RP3000299//”Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.”//0//2730bp//82%/D29766

C-NT2RP3000324

C-NT2RP3000341//”Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.”//1.5E-246//1124bp//99%/AF106622

C-NT2RP3000393//”Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.”//5.8E-266//1373bp//86%/AF061817

C-NT2RP3000441//”Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.”//3.40E-42//645bp//67%/AF098066

C-NT2RP3000449

C-NT2RP3000451

C-NT2RP3000456

C-NT2RP3000542

C-NT2RP3000561

C-NT2RP3000562//”Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.”//0//2165bp//99%//AF093097

C-NT2RP3000578//HES1 PROTEIN.//1.3E-22//229aa//27%//P35843

C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

C-NT2RP3000592

C-NT2RP3000622

C-NT2RP3000624

C-NT2RP3000685

C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140.//1.2E-166//305aa//99%//Q14153

C-NT2RP3000742//”1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-II I) (FRAGMENT).”//4.1E-165//371aa//49%//P10895

C-NT2RP3000753

C-NT2RP3000826

C-NT2RP3000865

C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426

C-NT2RP3001007

C-NT2RP3001055

C-NT2RP3001111//”Homo sapiens TRF-proximal protein mRNA, complete cds.”//1.50E-149//731bp//97%//AF097725

C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.8E-170//512aa//58%//P52737

C-NT2RP3001126

C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154

C-NT2RP3001232

C-NT2RP3001268//”Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.”//0//3606bp//99%//AF198358

C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.3E-99//669bp//83%//Y18101

C-NT2RP3001274//”Homo sapiens mRNA for KIAA1037 protein, partial cds.”//0//2254bp//99%//AB028960

C-NT2RP3001281

C-NT2RP3001297

C-NT2RP3001318

C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%/P51508

C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%//P32089

C-NT2RP3001374

C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%//P12270

C-NT2RP3001432

C-NT2RP3001447

C-NT2RP3001449//”Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG

islands, ESTs, STSS and GSSs, complete sequence."//0//1827bp//99%//AL03
1282

C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY
ANTIGEN MODIFIER 2).//3.2E-90//157aa//59%//P36371

C-NT2RP3001459

C-NT2RP3001527// "Human Sp140 protein (Sp140) mRNA, complete cds."//4.3E-
290//793bp//93%//U63420

C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//
9.10E-10//158aa//31%//Q10022

C-NT2RP3001580// "Mus musculus strain C57BL/J germ cell-less protein (Gcl
) mRNA, complete cds."//0//1730bp//85%//AF163665

C-NT2RP3001587// "Human anthracycline-associated resistance ARX mRNA, com
plete cds."//0//2617bp//99%//U35832

C-NT2RP3001589

C-NT2RP3001607

C-NT2RP3001608

C-NT2RP3001671// "Homo sapiens mRNA for KIAA0850 protein, complete cds."/
/0//2310bp//99%//AB020657

C-NT2RP3001672// "Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SC
MH1) mRNA, complete cds."//0//2836bp//99%//AF149046

C-NT2RP3001678

C-NT2RP3001688// "Homo sapiens glucocorticoid modulatory element binding
protein-1 (GMEB1) mRNA, complete cds."//0//1695bp//99%//AF099013

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.0000002
4//481aa//21%//P25386

C-NT2RP3001698

C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa/
/32%//P54356

C-NT2RP3001716

C-NT2RP3001752

C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.

8E-117//462aa//55%/P52272

C-NT2RP3001844

C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp//99%/AL050011

C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.1E-125//302aa//60%/P55347

C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1, 3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds."//0//1587bp//100%/AB000624

C-NT2RP3001931

C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%/P37709

C-NT2RP3002002

C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%/X86779

C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%/P39955

C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./5.30E-25//139aa//48%/Q09232

C-NT2RP3002045//Homo sapiens mRNA for KIAA0899 protein, partial cds."//0//3385bp//99%/AB020706

C-NT2RP3002056//Homo sapiens Rb binding protein homolog mRNA, partial cds."//0//2374bp//99%/AF083249

C-NT2RP3002062//Homo sapiens mRNA for KIAA0873 protein, partial cds."//0//3764bp//99%/AB020680

C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds."//4.1E-233//1896bp//69%/AF111423

C-NT2RP3002097

C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%/Q12

387

C-NT2RP3002142

C-NT2RP3002146

C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING
PROTEIN GST1-HS).//2.8E-253//474aa//93%/P15170

C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.9E-151//223a
a//91%/Q02614

C-NT2RP3002166

C-NT2RP3002181

C-NT2RP3002244

C-NT2RP3002248

C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%/P45978

C-NT2RP3002276

C-NT2RP3002304

C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE
DEAMINASE).//3.70E-43//318aa//37%/P05792

C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting
.//0//2276bp//99%/AJ133421

C-NT2RP3002566

C-NT2RP3002587

C-NT2RP3002590

C-NT2RP3002631

C-NT2RP3002650//”Mus musculus growth suppressor 1L (Gros1) mRNA, complet
e cds.”//0//2109bp//87%/AF165163

C-NT2RP3002663//”Homo sapiens putative glycolipid transfer protein mRNA,
complete cds.”//8.10E-263//1243bp//97%/AF103731

C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%/P1306

0

C-NT2RP3002763

C-NT2RP3002861

C-NT2RP3002911

C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2E-111//551aa//42%/Q04652

C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds."//0//2388bp//99%//AF152498

C-NT2RP3002988//Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds."//1.8E-292//1325bp//99%//AF080158

C-NT2RP3003008

C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds."//3.6E-83//807bp//72%//D88315

C-NT2RP3003204

C-NT2RP3003278

C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds."//0//2596bp//98%//L36983

C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds."//1.5e-310//1468bp//82%//AB033922

C-NT2RP3003302

C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds."//0//2476bp//99%//AF11765

7

C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052).//1.3E-35//178aa//44%//Q62191

C-NT2RP3003344

C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084

C-NT2RP3003377

C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds."//0//2133bp//85%/U09874

C-NT2RP3003433

C-NT2RP3003490//”Homo sapiens mRNA for KIAA0725 protein, partial cds.”//
0//2437bp//99%//AB018268

C-NT2RP3003491//”Drosophila melanogaster Pelle associated protein Pellin
o (Pli) mRNA, complete cds.”//5.6E-36//842bp//62%//AF091624

C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%//P17886

C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk
-1 gene).//0//2445bp//100%//AJ245820

C-NT2RP3004209//”Homo sapiens ubiquitin processing protease (Ubp-M) mRNA
, complete cds.”//0//2320bp//99%//AF126736

C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO
/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%
//P52734

C-NT2RP3004246

C-NT2RP3004258//”Homo sapiens ZIS1 mRNA, complete cds.”//0//1861bp//99%/
/AF065391

C-NT2RP3004262//”Homo sapiens heat shock protein hsp40-3 mRNA, complete
cds.”//2.4E-248//1126bp//100%//AF088982

C-NT2RP3004341

C-NT2RP3004378

C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1
E-66//364bp//93%//AJ007798

C-NT2RP3004428

C-NT2RP3004451

C-NT2RP3004454//”Homo sapiens mRNA for KIAA0448 protein, complete cds.”/
/0//2875bp//99%//AB007917

C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.6E-61//170aa//40%//Q01820

C-NT2RP3004498//”Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, co
mplete cds.”//2E-249//1777bp//80%//U83176

C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.9E-295//893bp//92%/
/Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%/P404
84

C-NT2RP3004534//"Mouse oncogene (ect2) mRNA, complete cds."//0//2075bp//
87%/L11316

C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%/P33755

C-NT2RP4000907//"Mouse NLRR-1 mRNA for leucine-rich-repeat protein, comp
lete cds."//0//2127bp//86%/D45913

C-NT2RP4001029//"Mus domesticus nuclear binding factor NF2d9 mRNA, compl
ete cds."//0//1711bp//90%/U20086

C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PRO
TEIN.//0.000016//186aa//29%/O24076

C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%/P35844

C-NT2RP4001442

C-NT2RP4001529//"Mus domesticus nuclear binding factor NF2d9 mRNA, compl
ete cds."//1.70E-255//1148bp//90%/U20086

C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-
45//310aa//27%/P12868

C-OVARC1000106//"TROPOMYOSIN 1, FUSION PROTEIN 33."//0.000032//165aa//27
%/P49455

C-OVARC1000198

C-OVARC1000682//"PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,
2-MANNOSIDASE 1B)."//1.1E-209//293aa//95%/P39098

C-OVARC1000703

C-OVARC1000722//"Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltr
ansferase mRNA, complete cds."//0//759bp//98%/AF038661

C-OVARC1000730

C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%

//P25159
 C-OVARC1000781
 C-OVARC1000787
 C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2
 .8E-258//1183bp//99%/Y17711
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%/P08199
 C-OVARC1000850//"Homo sapiens PB39 mRNA, complete cds."//0//2095bp//99%/
 /AF045584
 C-OVARC1000862//M.musculus mRNA for FT1.//5.9E-226//1498bp//81%/Z67963
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%/P404
 84
 C-OVARC1000883
 C-OVARC1000886
 C-OVARC1000912
 C-OVARC1000915//"Homo sapiens histone deacetylase 5 mRNA, complete cds."
 //1.60E-121//591bp//97%/AF132608
 C-OVARC1000924
 C-OVARC1000964
 C-OVARC1000984
 C-OVARC1001004
 C-OVARC1001010
 C-OVARC1001011
 C-OVARC1001032
 C-OVARC1001044
 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//9
 8%/P43490
 C-OVARC1001068//"Homo sapiens Era GTPase A protein (HERA-A) mRNA, partia
 l cds."//0//1819bp//99%/AF082657
 C-OVARC1001074

C-OVARC1001092//”Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).”//2E-214//769bp//97%//AJ005897

C-OVARC1001107//”Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.”//6.1E-276//594bp//98%//AF167572

C-OVARC1001154//”Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.”//2.3E-296//1561bp//93%//AF055008

C-OVARC1001161

C-OVARC1001167

C-OVARC1001170

C-OVARC1001171//”Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.”//5.7E-151//436bp//92%//U94855

C-OVARC1001173

C-OVARC1001176

C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510

C-OVARC1001188

C-OVARC1001232//”CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).”//5.10E-22//83aa//37%//Q10568

C-OVARC1001270

C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//224aa//26%//P25976

C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444

C-OVARC1001344

C-OVARC1001369

C-OVARC1001372//”Homo sapiens mRNA for KIAA0897 protein, partial cds.”//0//840bp//97%//AB020704

C-OVARC1001391

C-OVARC1001399

C-OVARC1001417//”Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds.”//0//1715bp//99%//AF135802

C-OVARC1001419//”Homo sapiens GOK (STIM1) mRNA, complete cds.”//4.9E-48//586bp//69%//U52426

C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111

C-OVARC1001453

C-OVARC1001476//”Mus musculus YGR163w mRNA homologue, complete cds.”//1.80E-187//510bp//89%//AB017616

C-OVARC1001480

C-OVARC1001489

C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161

C-OVARC1001525

C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081

C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retroseudogene.//0//1167bp//100%//AF031165

C-OVARC1001600

C-OVARC1001610//”Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.”//0//1870bp//99%//AF068302

C-OVARC1001702

C-OVARC1001703//”Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.”//3.5E-16//399bp//61%//AF133670

C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1B).//2.80E-10//106aa//38%//Q62267

C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106

C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%

//Q13796

C-OVARC1001731//”TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.”//4E-12
2//282aa//85%//P08942

C-OVARC1001745

C-OVARC1001762//”N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TER
MINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).”//6.4E-85//514aa//34%//P12945

C-OVARC1001766//”Homo sapiens eukaryotic translation initiation factor e
IF3, p35 subunit mRNA, complete cds.”//0//963bp//99%//U97670

C-OVARC1001767//”Homo sapiens mRNA for KIAA0675 protein, complete cds.”/
/0//2083bp//99%//AB014575

C-OVARC1001768

C-OVARC1001791

C-OVARC1001795

C-OVARC1001802

C-OVARC1001809//”Mus musculus sphingosine kinase (SPHK1a) mRNA, partial
cds.”//2.7E-190//1624bp//76%//AF068748

C-OVARC1001828

C-OVARC1001846

C-OVARC1001861

C-OVARC1001879

C-OVARC1001880

C-OVARC1001883

C-OVARC1001916

C-OVARC1001928

C-OVARC1001942//”N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TER
MINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).”//3.1E-81//497aa//35%//P12945

C-OVARC1001943//”Mus musculus DEBT-91 mRNA, complete cds.”//0//2035bp//8
7%//AF143859

C-OVARC1001950

C-OVARC1001987// "Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds."//2.3E-220//652bp//84%//AF061817

C-OVARC1002050// "Homo sapiens mRNA for actin binding protein ABP620, complete cds."//0//1019bp//99%//AB029290

C-OVARC1002082

C-OVARC1002107

C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//035913

C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955

C-OVARC1002156

C-OVARC1002158

C-PLACE1000004// "Homo sapiens IDN3-B mRNA, complete cds."//0//2365bp//99%//AB019602

C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643

C-PLACE1000048

C-PLACE1000050

C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154

C-PLACE1000081// "Human SEC7 homolog Tic (TIC) mRNA, complete cds."//0//2077bp//99%//U63127

C-PLACE1000094

C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8E-62//158aa//81%//P20290

C-PLACE1000214

C-PLACE1000236

C-PLACE1000246

C-PLACE1000292

C-PLACE1000308
C-PLACE1000332
C-PLACE1000453
C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60
E-47//207aa//46%/P51522
C-PLACE1000599
C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%/P52918
C-PLACE1000653// "Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
complete cds."//0//1992bp//99%/AF180371
C-PLACE1000656// "Homo sapiens mRNA for JM4 protein, complete CDS (clone
IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))."//2.1E-277//1260bp//99%
//AJ005896
C-PLACE1000706// "Homo sapiens transcriptional intermediary factor 1 gamm
a mRNA, complete cds."//0//1366bp//99%/AF119043
C-PLACE1000712
C-PLACE1000749
C-PLACE1000769// "Homo sapiens CGI-18 protein mRNA, complete cds."//0//19
85bp//98%/AF132952
C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO
/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%
//P52734
C-PLACE1000849
C-PLACE1000856// "Homo sapiens mRNA for KIAA0974 protein, partial cds."//
0//1310bp//100%/AB023191
C-PLACE1000931
C-PLACE1000987// "Homo sapiens mRNA for KIAA0724 protein, complete cds."/
/0//1749bp//99%/AB018267
C-PLACE1001010
C-PLACE1001015

C-PLACE1001024
 C-PLACE1001062// "Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence."//2.7E-32//470bp//71%//AC006020
 C-PLACE1001104
 C-PLACE1001168
 C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%//Q13496
 C-PLACE1001185// "Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//1668bp//99%//AB023160
 C-PLACE1001238// "Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//2E-202//1333bp//80%//D14336
 C-PLACE1001280
 C-PLACE1001294//M.musculus GEG-154 mRNA.//4.3E-221//1057bp//78%//X71642
 C-PLACE1001304// "Homo sapiens zinc finger protein dp mRNA, complete cds."//0//2421bp//99%//AF153201
 C-PLACE1001311
 C-PLACE1001323
 C-PLACE1001351
 C-PLACE1001414
 C-PLACE1001440
 C-PLACE1001456
 C-PLACE1001517// "Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds."//4.60E-112//392bp//87%//AB002137
 C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809
 C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//P51523
 C-PLACE1001634
 C-PLACE1001640
 C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-6

6//174aa//45%/P91408
C-PLACE1001705
C-PLACE1001716
C-PLACE1001720
C-PLACE1001745
C-PLACE1001748//”Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds
.”//0//2602bp//99%/AF061243
C-PLACE1001771//Homo sapiens mRNA for transient receptor potential prote
in TRP6.//0//2900bp//99%/AJ006276
C-PLACE1001799
C-PLACE1001845//”Mus musculus cyclin ania-6a mRNA, complete cds.”//3.30E
-31//925bp//62%/AF159159
C-PLACE1001897
C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E
-58//112aa//100%/076094
C-PLACE1002157
C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX C
OMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%/P32591
C-PLACE1002227
C-PLACE1002259
C-PLACE1002319
C-PLACE1002395//”Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, comple
te cds.”//7.9E-100//966bp//75%/AB030505
C-PLACE1002477
C-PLACE1002493//”Homo sapiens signal transducing adaptor molecule 2A (ST
AM2) mRNA, complete cds.”//1.7E-113//545bp//98%/AF042273
C-PLACE1002500
C-PLACE1002514
C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.2E-152//289aa//96%/P70396

C-PLACE1002537

C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%/P45890

C-PLACE1002583//”GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).”//5.6E-34//76aa//98%/P39087

C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%/P45340

C-PLACE1002625

C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.5E-278//543aa//92%/Q28046

C-PLACE1002768

C-PLACE1002782//”Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.”//3.8E-43//385bp//77%/U50927

C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%/P53973

C-PLACE1002853

C-PLACE1002908//”Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.”//0//1654bp//99%/AB028600

C-PLACE1002962

C-PLACE1002968

C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%/Q49091

C-PLACE1003025

C-PLACE1003027//”Homo sapiens mRNA for KIAA0516 protein, partial cds.”//2.1e-314//1417bp//100%/AB011088

C-PLACE1003044//”Homo sapiens mRNA for KIAA0829 protein, partial cds.”//0//1382bp//96%/AB020636

C-PLACE1003176

C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%/Q15391

C-PLACE1003256

C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa//47%/P21541

C-PLACE1003343

C-PLACE1003361

C-PLACE1003366//”Homo sapiens otoferlin (OTOF) mRNA, complete cds.”//1.4E-78//542bp//67%//AF107403

C-PLACE1003373

C-PLACE1003375

C-PLACE1003394//”Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.”//2.30E-150//774bp//94%//M83680

C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.3E-40//278aa//36%//P40556

C-PLACE1003454

C-PLACE1003478

C-PLACE1003516

C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136

C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//Q09475

C-PLACE1003528

C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//7.7E-68//404aa//33%//P32802

C-PLACE1003566

C-PLACE1003584

C-PLACE1003593

C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.00000023//82aa//35%//Q02516

C-PLACE1003618

C-PLACE1003638

C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%/P52742

C-PLACE1003760//”Homo sapiens tetraspanin TM4-A mRNA, complete cds.”//5.

2E-289//1313bp//97%/AF133423

C-PLACE1003768

C-PLACE1003795

C-PLACE1003886

C-PLACE1003888//”Homo sapiens mRNA for KIAA1092 protein, partial cds.”//

0//2057bp//99%/AB029015

C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//584aa//74%/P17812

C-PLACE1003915//”PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE- -TRNA LIGASE) (ARGRS).”//2.4E-108//581aa//40%/Q05506

C-PLACE1004118

C-PLACE1004256//”Mus musculus short coiled coil protein SCOCO (Scoc) mRNA A, complete cds.”//2E-93//960bp//76%/AF115778

C-PLACE1004274

C-PLACE1004284

C-PLACE1005331

C-PLACE1005739//Homo sapiens mRNA: cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//99%/AL050267

C-PLACE1005828

C-PLACE1005876//”CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).”//0//730aa//99%/Q10568

C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%/P54069

C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//30%/P98110

C-PLACE1007053

C-PLACE1007068

C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%
//Q04652

C-PLACE1009921

C-PLACE1010401

C-PLACE1010856

C-PLACE1010857

C-PLACE1010917

C-PLACE1010925

C-PLACE1010926//”Homo sapiens mRNA for KIAA0554 protein, partial cds.”//
0//1160bp//100%//AB011126

C-PLACE1010942//”Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.”//0//1440bp//99%//AF114487

C-PLACE1010944

C-PLACE1010954

C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890

C-PLACE1011026

C-PLACE1011046//”1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).”//0//646aa//97%//P10894

C-PLACE1011054

C-PLACE1011057

C-PLACE1011109//”ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).”//
/1.50E-22//63aa//88%//Q07803

C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532

C-PLACE1011133

C-PLACE1011143

C-PLACE1011165

C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100
%/P03830

C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//3.2E-12//212aa//2
9%/Q03326

C-PLACE1011221

C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp56
40043).//0//2487bp//99%/AL050390

C-PLACE1011325

C-PLACE1011332//”Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
complete cds.”//7.2E-151//697bp//99%/AF102265

C-PLACE1011340//”Homo sapiens IDN3-B mRNA, complete cds.”//1.20E-74//380
bp//97%/AB019602

C-PLACE1011399//”Homo sapiens CGI-72 protein mRNA, complete cds.”//3.2E-
90//427bp//99%/AF151830

C-PLACE1011433//”Homo sapiens mRNA for KIAA0530 protein, partial cds.”//
0//1946bp//99%/AB011102

C-PLACE1011452

C-PLACE1011465

C-PLACE1011472//”Homo sapiens mRNA for KIAA0712 protein, complete cds.”/
/0//2022bp//99%/AB018255

C-PLACE1011477//”Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.
”//0//2040bp//99%/AF065482

C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSO
R (CTPT).//4.90E-11//147aa//32%/P52178

C-PLACE1011520

C-PLACE1011563

C-PLACE1011567

C-PLACE1011576//”Human Kruppel related zinc finger protein (HTF10) mRNA,
complete cds.”//0//1791bp//82%/L11672

C-PLACE1011586
 C-PLACE1011643
 C-PLACE1011649
 C-PLACE1011664//CROOKED NECK PROTEIN.//1.6E-187//505aa//64%/P17886
 C-PLACE1011682
 C-PLACE1011719
 C-PLACE1011729
 C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//0//1490bp//99%/AL050287
 C-PLACE1011874
 C-PLACE1011875//"Homo sapiens mRNA for KIAA0580 protein, partial cds."//4.1E-112//524bp//100%/AB011152
 C-PLACE1011923//"Homo sapiens serum-inducible kinase mRNA, complete cds."//0//2782bp//99%/AF059617
 C-PLACE1011982
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.6E-42//104aa//49%/Q09475
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.1E-116//364aa//45%/P42566
 C-PLACE2000017
 C-PLACE2000021//"Homo sapiens TRF1-interacting ankyrin-related ADP-ribosom e polymerase mRNA, complete cds."//2.7E-107//981bp//74%/AF082556
 C-PLACE2000047
 C-PLACE2000062//"Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347."//6.3E-166//656bp//94%/AB015629
 C-PLACE2000100
 C-PLACE2000111
 C-PLACE2000172

C-PLACE2000187

C-PLACE2000216// "Dog nonerythroid beta-spectrin mRNA, 3' end."//3.2E-253
//1799bp//83%//L02897

C-PLACE2000246// "Homo sapiens mRNA for KIAA0795 protein, partial cds."//
4.60E-172//796bp//99%//AB018338

C-PLACE2000317

C-PLACE2000341// "Homo sapiens sodium-dependent multivitamin transporter
(SMVT) mRNA, complete cds."//0//1554bp//99%//AF069307

C-PLACE2000366

C-PLACE2000373//F-SPONDIN PRECURSOR.//8.6E-16//371aa//28%//P35446

C-PLACE2000394

C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.
1.3.48).//6.3E-37//90aa//98%//P10586

C-PLACE2000411// "Homo sapiens mRNA for KIAA1037 protein, partial cds."//
0//2515bp//99%//AB028960

C-PLACE2000425

C-PLACE2000427//PROBABLE HELICASE MOT1.//1.2E-26//200aa//27%//P32333

C-PLACE2000433

C-PLACE2000438// "POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1
.41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPT
IDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)."//2.1E-86//348aa//
41%//Q10472

C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN
) .//2.5E-25//165aa//40%//P33450

C-PLACE2000477// "Homo sapiens putative secreted protein (ZSIG11) mRNA, c
omplete cds."//6.7E-127//671bp//94%//AF072733

C-PLACE3000009

C-PLACE3000020// "Homo sapiens type III adenylyl cyclase (AC-III) mRNA, c
omplete cds."//0//2253bp//99%//AF033861

C-PLACE3000103
 C-PLACE3000142
 C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205
 C-PLACE3000156
 C-PLACE3000157
 C-PLACE3000197
 C-PLACE3000208
 C-PLACE3000226//”Homo sapiens mRNA for KIAA0962 protein, partial cds.”//
 0//4805bp//99%//AB023179
 C-PLACE3000242//”Homo sapiens mRNA for KIAA1114 protein, complete cds.”/
 /0//2786bp//96%//AB029037
 C-PLACE3000363
 C-PLACE3000405
 C-PLACE3000416//”Homo sapiens mRNA for actin binding protein ABP620, com
 plete cds.”//1.80E-141//565bp//98%//AB029290
 C-PLACE3000477
 C-PLACE4000106//”Homo sapiens mRNA for KIAA0462 protein, partial cds.”//
 0//6702bp//99%//AB007931
 C-PLACE4000323
 C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (U
 P-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
 C-PLACE4000369//”Homo sapiens mRNA for KIAA1025 protein, partial cds.”//
 0//4830bp//99%//AB028948
 C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp43
 4C212).//0//2565bp//99%//AL080196
 C-PLACE4000558//”Homo sapiens mRNA for KIAA0729 protein, partial cds.”//
 0//1051bp//97%//AB018272
 C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED
 PROTEIN 1) (UEGF-1).//9.3E-70//226aa//52%//P10079